

Protein Sequence Searches - February 2005

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<http://www.pir.uniprot.org/database/archive.shtml>

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When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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Range: from to
 Features:
 ☐ SNP
 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [CAC07879](#). Reports unnamed protein p...[gi:10046113]

[BLink](#), [Links](#)

LOCUS CAC07879 417 aa linear UNA 24-NOV-2000
 DEFINITION unnamed protein product [unidentified].
 ACCESSION CAC07879
 VERSION CAC07879.1 GI:10046113
 DBSOURCE embl accession [AX022514.1](#)
 KEYWORDS .

SOURCE unidentified
 ORGANISM [unidentified](#)
 unclassified.
 REFERENCE 1
 AUTHORS Flegel,W.A. and Wagner,F.F.
 TITLE Novel nucleic acid molecules correlated with the rhesus weak d phenotype
 JOURNAL Patent: WO 9937763-A 29-JUL-1999;
 FLEGEL WILLY A (DE) ; WAGNER FRANZ F (DE) ; DRK BLUTSPENDEDIENST
 BADEN WUE (DE)

FEATURES Location/Qualifiers
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 /db_xref="taxon:32644"
 Protein 1..417
 /name="unnamed protein product"
 CDS 1..417
 /coded_by="AX022514.1:1..1254"

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 61 glgfltssfr rhswssvafn lfmlalgvqw ailldgflsq fpsgkvvitl fsirlatmsa
 121 lsvlisvdav lgkvnlaqlv vmvlvevtal gnrmvisni fntdyhmnm hiyvfaayfg
 181 lsvawclpkp lpegtdkdq tatipslsam lgalflwmfw psfnsallrs pierknafn
 241 tyyavavsvv taisgsslah pggkisktyv hsavlaggva vgtschlips pwlamvlgv
 301 aglisvggak ylpgccnrvl giphssimgy nfslglgllge iiyivllvld tvgagngmig
 361 fqvllsigel slaivialts glltglllnl kiwkapheak yfddqvfwkf phlavgf
 //

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Feb 9 2005 14:31:10

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 13:13:49 ; Search time 24 Seconds
(without alignments)
1297.027 Million cell updates/sec

Title: CAC07879

Perfect score: 2124

Sequence: 1 MSCKYRSVRGRLPLCALTL.....EAKYFDQVFWKPHLAVGF 417

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :
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3: /cgnt2_6/prodata/1/1aa/6A COMB .pep.*
4: /cgnt2_6/prodata/1/1aa/6B COMB .pep.*
5: /cgnt2_6/prodata/1/1aa/PCITUS COMB .pep.*
6: /cgnt2_6/prodata/1/1aa/backfile1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1833	86.3	417	1 US-08-553-888A-3	Sequence 3, Appl1
2	552.5	26.0	418	4 US-09-949-016-7328	Sequence 7328, Ap
3	497	23.4	487	4 US-09-949-016-9649	Sequence 9649, Ap
4	202	9.5	145	4 US-09-461-325-438	Sequence 438, App
5	202	9.5	145	4 US-10-012-542-438	Sequence 438, App
6	202	9.5	145	4 US-10-115-123-438	Sequence 438, App
7	142	6.7	308	4 US-09-461-325-437	Sequence 437, App
8	142	6.7	308	4 US-10-012-542-437	Sequence 437, App
9	142	6.7	308	4 US-10-115-123-437	Sequence 437, App
10	117.5	5.6	633	4 US-09-248-796A-20407	Sequence 20407, A
11	114	5.4	801	4 US-09-710-379-2020	Sequence 2020, Ap
12	114	5.4	808	4 US-09-134-001C-3105	Sequence 3105, Ap
13	113.5	5.3	447	4 US-09-489-039A-7527	Sequence 7527, Ap
14	110	5.2	800	4 US-09-134-001C-5655	Sequence 5655, Ap
15	109.5	5.2	407	4 US-09-489-039A-10855	Sequence 10855, A
16	109.5	5.2	464	4 US-09-252-991A-18525	Sequence 18525, A
17	109	5.1	449	4 US-09-543-681A-6546	Sequence 6546, Ap
18	108.5	5.1	447	4 US-10-162-012-29	Sequence 29, Appl
19	108.5	5.1	509	4 US-09-252-991A-30864	Sequence 30864, A
20	108.5	5.1	518	4 US-09-252-991A-31586	Sequence 31586, A
21	107	5.0	447	4 US-09-328-352-6978	Sequence 6978, Ap
22	107	5.0	447	4 US-09-489-039A-11893	Sequence 11893, A
23	107	5.0	448	4 US-09-583-110-4040	Sequence 4040, Ap
24	107	5.0	452	4 US-09-107-433-5105	Sequence 5105, Ap
25	106.5	5.0	478	4 US-09-328-352-7771	Sequence 7771, Ap
26	106.5	5.0	517	4 US-09-252-991A-19322	Sequence 19322, A
27	104.5	4.9	437	3 US-09-134-001C-4808	Sequence 4808, Ap

28	104	4.9	401	4 US-09-328-352-5448	Sequence 5448, Ap
29	104	4.9	465	4 US-09-603-208A-258	Sequence 258, App
30	103	4.8	484	4 US-09-252-991A-30013	Sequence 30013, A
31	103	4.8	484	4 US-09-489-039A-11054	Sequence 11054, A
32	101.5	4.8	483	4 US-09-107-532A-4123	Sequence 4123, App
33	101	4.8	181	4 US-09-461-325-196	Sequence 196, App
34	101	4.8	181	4 US-10-012-542-196	Sequence 196, App
35	101	4.8	181	4 US-10-115-123-196	Sequence 196, App
36	101	4.8	448	4 US-09-543-681A-7245	Sequence 7245, Ap
37	101	4.8	470	4 US-09-489-039A-8514	Sequence 8514, Ap
38	101	4.8	511	4 US-09-543-681A-7476	Sequence 7476, Ap
39	100.5	4.7	486	4 US-10-033-109-12	Sequence 12, Appl
40	100.5	4.7	1323	4 US-09-270-767-46728	Sequence 46728, A
41	100	4.7	418	4 US-09-489-039A-12883	Sequence 12883, A
42	100	4.7	437	4 US-09-830-433A-12	Sequence 12, Appl
43	100	4.7	548	4 US-09-328-352-6605	Sequence 6605, Ap
44	100	4.7	565	4 US-09-602-787A-616	Sequence 616, App
45	99.5	4.7	1607	4 US-09-902-540-16765	Sequence 16765, A

ALIGNMENTS

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RESULT 1
US-08-553-888A-3
; Sequence 3, Application US/08553888A
; Patent No. 5723293
; GENERAL INFORMATION:
; APPLICANT: Huang
; TITLE OF INVENTION: DIAGNOSTIC METHOD AND KIT FOR
; TITLE OF INVENTION: DETERMINING RH BLOOD GROUP GENOTYPE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: USA
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553, 888A
; FILING DATE: 11/06/95
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: O'Dea, Sean W.
; REGISTRATION NUMBER: 37690
; REFERENCE/DOCKET NUMBER: 454-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 417 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-553-888A-3

Query Match      86.3%; Score 1833; DB 1; Length 417;
Best Local Similarity 88.7%; Pred. No. 4.6e-184;
Matches 370; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY      1 MSCKYRSVRGRLPLCALTLLEFFFTYDASLEBQKGVASVYGODLTWAAI 60
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Db      1 MSCKYRSVRGRLPLCALTLLEFFFTYDASLEBQKGVASVYGODLTWAAI 60
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      61 GIGFLTSSFRHSSVAENLFWALGVQVAILLDGLSQPSGKVVITLFSIWLATMSA 120
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Db      61 GIGFLLTNSFRHSSWSSVAFNLFWLALGVOMAILLDFGLSQPPGKVITLFSIRLATMSA 120
Qy      121 LSVLTSVDAVLGVNLAOLVWVVLVEVTDLGNLRWVTSINIENTDYMNMHIIYVPAAYFG 180
      121 MSVLSAGAVLGVNLAOLVWVVLVEVTDLGNLRWVTSINIENTDYMNMHIIYVPAAYFG 180
Qy      181 LTVAMCLPKRPLEGTEEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPIERKNAYEN 240
      181 LTVAMCLPKRPLEGTEEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPIERKNAYEN 240
Db      241 TYVAAVSVVTAISSGSLAHPOGKISKITYGHSAYLPEGVAVDTSCHLIPSPWLPITVLGV 300
      241 TYVAAVSVVTAISSGSLAHPOGKISKITYGHSAYLPEGVAVDTSCHLIPSPWLPITVLGV 300
Qy      301 AGLLISVGAKYLPGCCNRVLGIPIHSSINGVNSLLGLEELIYITVLVLDYMGANGMIG 360
      301 AGLLISVGAKYLPGCCNRVLGIPIHSSINGVNSLLGLEELIYITVLVLDYMGANGMIG 360
Db      361 FOVLISIGELSLAIYIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
      361 FOVLISIGELSLAIYIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
Qy      361 FOVLISIGELSLAIYIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
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RESULT 2
US-09-949-016-7328
; Sequence 7328, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7328
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7328

Query Match      26.0%; Score 552.5; DB 4; Length 418;
Best Local Similarity 34.1%; Pred. No. 2.4e-49;
Matches 140; Conservative 76; Mismatches 171; Indels 21; Gaps 7;

Qy      14 PLCAITLLEALLILFYFFTHY--DASLEDQKGLVASVOG-----ODLTVMMAIGL 62
      14 PLCAITLLEALLILFYFFTHY--DASLEDQKGLVASVOG-----ODLTVMMAIGL 62
Db      15 PLMAIVLEIMIVLFGFVEYETDQVLEQDINTKPTDWCIFPELYLPFDVHVMIFVGR 74
      15 PLMAIVLEIMIVLFGFVEYETDQVLEQDINTKPTDWCIFPELYLPFDVHVMIFVGR 74
Qy      63 GFLTSSFRHSSWSSVAFNLFWLALGVOMAILLDFGLSQPPGKVITLFSIRLATMSA 122
      63 GFLTSSFRHSSWSSVAFNLFWLALGVOMAILLDFGLSQPPGKVITLFSIRLATMSA 122
Db      75 GFLMTFLKKTGFSSVGNLVLVAALGLQWGTIVGIL--QSQGQKFNIGIKIMINADPSAAT 133
      75 GFLMTFLKKTGFSSVGNLVLVAALGLQWGTIVGIL--QSQGQKFNIGIKIMINADPSAAT 133
Qy      123 VLISVDAVLGVNLAOLVWVVLVEVTDLGNLRWVTSINIENTDYMNMHIIYVPAAYFG 182
      123 VLISVDAVLGVNLAOLVWVVLVEVTDLGNLRWVTSINIENTDYMNMHIIYVPAAYFG 182
Db      134 VLISFGAVIGKTSPTQWLIMTIIIEVFAFNEVLESEIFASDIGASMTIHAFGAYFG 193
      134 VLISFGAVIGKTSPTQWLIMTIIIEVFAFNEVLESEIFASDIGASMTIHAFGAYFG 193
Qy      183 VAMCLPKRPLEGTEEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPIERKNAYEN 242
      183 VAMCLPKRPLEGTEEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPIERKNAYEN 242
Db      194 VAGILRSGLRKHENESEAYVSDLPFAMIGTLPFLMFMFSPNSAIPGDKOCRAIVNTY 253
      194 VAGILRSGLRKHENESEAYVSDLPFAMIGTLPFLMFMFSPNSAIPGDKOCRAIVNTY 253
Qy      243 YAVAASVVTAISSGSLAHPOGKISKITYGHSAYLPEGVAVDTSCHLIPSPWLPITVLGV 302
      243 YAVAASVVTAISSGSLAHPOGKISKITYGHSAYLPEGVAVDTSCHLIPSPWLPITVLGV 302
Db      254 FSLAACVTLTFASSLVHRKGLNMVHIOVATLAGVAVAGTCADMAIHFGGMIIGSIA 313
      254 FSLAACVTLTFASSLVHRKGLNMVHIOVATLAGVAVAGTCADMAIHFGGMIIGSIA 313
Qy      303 LISVRGAKYLPGCCNRVLGIPIHSSINGVNSLLGLEELIYITVLVLDYMGANGMIG 361
      303 LISVRGAKYLPGCCNRVLGIPIHSSINGVNSLLGLEELIYITVLVLDYMGANGMIG 361

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Db      314 MSVLSAGAVLGVNLAOLVWVVLVEVTDLGNLRWVTSINIENTDYMNMHIIYVPAAYFG 180
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      362 FOVLISIGELSLAIYIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPHLAVGF 417
Db      370 QA-----AALSSIGTAVVGSLMTGLIKLPWMQPSQONCYDSDSVYWKOP 415
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RESULT 3
US-09-949-016-9649
; Sequence 9649, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9649
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9649

Query Match      23.4%; Score 497; DB 4; Length 487;
Best Local Similarity 29.4%; Pred. No. 2.1e-43;
Matches 129; Conservative 77; Mismatches 183; Indels 50; Gaps 8;

Qy      13 LPLCAITLLEALLILFYFFTHYD-----ASLEDQKGLVASVOGODLTVMMAIGL 58
      13 LPLCAITLLEALLILFYFFTHYD-----ASLEDQKGLVASVOGODLTVMMAIGL 58
Db      19 LPLTCLLQVIMVILFGFVRYDPEADAHMWSERTKQLSDMESEFYRYPSPQDVHVMV 78
      19 LPLTCLLQVIMVILFGFVRYDPEADAHMWSERTKQLSDMESEFYRYPSPQDVHVMV 78
Qy      59 AIGLGLTSSFRHSSWSSVAFNLFWLALGVOMAILLDFGLSQPPGKVITLFSIRLATMSA 118
      59 AIGLGLTSSFRHSSWSSVAFNLFWLALGVOMAILLDFGLSQPPGKVITLFSIRLATMSA 118
Db      79 FVGFGLMTFLQRYGFSAVGFEFLAAGIQWALMQWHPFLQDRYIVGVEVNLINDF 138
      79 FVGFGLMTFLQRYGFSAVGFEFLAAGIQWALMQWHPFLQDRYIVGVEVNLINDF 138
Qy      119 SALSVLISVDAVLGVNLAOLVWVVLVEVTDLGNLRWVTSINIENTDYMNMHIIYVPAAY 178
      119 SALSVLISVDAVLGVNLAOLVWVVLVEVTDLGNLRWVTSINIENTDYMNMHIIYVPAAY 178
Db      139 CVASVCVAFGAVLGVSPIDQLIMTFQVTLFAVNEFLIMLKVKAGSGMTIHTFGAY 198
      139 CVASVCVAFGAVLGVSPIDQLIMTFQVTLFAVNEFLIMLKVKAGSGMTIHTFGAY 198
Qy      179 FGLTVAMCLPKRPLEGTEEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPIERKNAY 238
      179 FGLTVAMCLPKRPLEGTEEDNDQORATIPSLSAMLGALFLMMPRPVSNSALLRSPIERKNAY 238
Db      199 FGLTVTRILYHRNLEQSKERQNSVYQSDLPFAMIGTLPFLMFMFSPNSAISTHSGSQRRA 258
      199 FGLTVTRILYHRNLEQSKERQNSVYQSDLPFAMIGTLPFLMFMFSPNSAISTHSGSQRRA 258
Qy      239 FRTYVAASVVTAISSGSLAHPOGKISKITYGHSAYLPEGVAVDTSCHLIPSPWLPITVLG 298
      239 FRTYVAASVVTAISSGSLAHPOGKISKITYGHSAYLPEGVAVDTSCHLIPSPWLPITVLG 298
Db      259 INTYGSILAACVLTVAISSALHKKGKLDVHIOVATLAGVAVAGTAAEMMLMPYCALIIG 318
      259 INTYGSILAACVLTVAISSALHKKGKLDVHIOVATLAGVAVAGTAAEMMLMPYCALIIG 318
Qy      299 LVAGLISVRGAKYLPGCCNRVLGIPIHSSINGVNSLLGLEELIYITVLVLDYMGANGMIG 369
      299 LVAGLISVRGAKYLPGCCNRVLGIPIHSSINGVNSLLGLEELIYITVLVLDYMGANGMIG 369
Db      319 FVCGIISTGLGVYITLPLFLESRLHIQDTGGINNHGIP-----GIGGIVGAVPAAS 369
      319 FVCGIISTGLGVYITLPLFLESRLHIQDTGGINNHGIP-----GIGGIVGAVPAAS 369
Qy      347 LVLDTVGANGMT-----GF-----QVLISIGELSLAIYIALTSGLLTALLNLKIR 392
      347 LVLDTVGANGMT-----GF-----QVLISIGELSLAIYIALTSGLLTALLNLKIR 392
Db      370 ASLEVYVK-EGLVASDFQGFNGDWTARTQOKPQIYGLVLTLMALMNGIIVGLILRLPF 428
      370 ASLEVYVK-EGLVASDFQGFNGDWTARTQOKPQIYGLVLTLMALMNGIIVGLILRLPF 428
Qy      393 RKAPHEAKYFDDQVFWKPHLAVGF 411
      393 RKAPHEAKYFDDQVFWKPHLAVGF 411
Db      429 WQPSDENCEDAVYWMEMP 447
      429 WQPSDENCEDAVYWMEMP 447

RESULT 4
US-09-461-325-438
; Sequence 438, Application US/09461325A

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: Patent No.66475753
:
: GENERAL INFORMATION:
:
: APPLICANT: Ruben et al.
:
: TITLE OF INVENTION: 94 Human Secreted Proteins
:
: FILE REFERENCE: P2029P1
:
: CURRENT APPLICATION NUMBER: US/09/461,325A
:
: EARLIER FILING DATE: 1999-12-14
: EARLIER APPLICATION NUMBER: PCT/US99/13418
:
: EARLIER FILING DATE: 1999-06-15
: EARLIER APPLICATION NUMBER: 60/089,507
:
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,508
:
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,509
:
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,510
:
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/090,112
:
: EARLIER FILING DATE: 1998-06-22
: EARLIER APPLICATION NUMBER: 60/090,113
:
: EARLIER FILING DATE: 1998-06-22
: NUMBER OF SEQ ID NOS: 532
:
: SOFTWARE: PatentIn Ver. 2.0
:
: SEQ ID NO 438
:
: LENGTH: 145
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: OS-09-461-325-438

```

[illegible][illegible]

QY	142	MVLVEVDTGLDKRWKVISINFTVDHMMNMHTYVFAAYGLTVANCLPKPFLPEGTEEDNQ	201	
DB	1	MTFFQVTLFAVNEFLINLLKLVKQAGSGMTIHTGAYGLTVTRILYRNLQSKTERONS	60	
QY	202	ATIPSLAMLGALFLIMFSPVNSALTRSPIERKNAVENTFYAAVSVTAISGSLAHP	261	
DB	61	VYQSLEFLMNIETLFLPMYTPSPFNSAISVHSGDSQRRAINTYCSLAACVLTSAISSALHK	120	
QY	262	QGIKISKTYGSHAVLPPEGVAVDTS	284	
DB	121	KGKLDVMHIQNTATLAGVAVGTA	143	

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

Query Match

Best Local Similarity 34.3%; Pred. NO. 3.7e-13;

Matches 49; Conservative 24; Mismatches 70; Indels 0; Gaps 0;

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

Sequence 438, Application US/10115123

Patent No. 6774216

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins

FILE REFERENCE: P2029630APID2

CURRENT APPLICATION NUMBER: US/10/115.123

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: PCT/US99/13418

PRIOR FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: 60/089,507

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,508

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,509

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,510

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/090,112

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090,113

PRIOR FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 438

LENGTH: 145

TYPE: PRT

ORGANISM: Homo sapiens

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

US-09-461-325-437

US-09-461-325-437

US-09-461-325-437

Query Match

Best Local Similarity 34.3%; Pred. NO. 3.7e-13;

Matches 49; Conservative 24; Mismatches 70; Indels 0; Gaps 0;

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

Sequence 438, Application US/10115123

Patent No. 6774216

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins

FILE REFERENCE: P2029630APID2

CURRENT APPLICATION NUMBER: US/10/115.123

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: PCT/US99/13418

PRIOR FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: 60/089,507

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,508

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,509

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,510

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/090,112

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090,113

PRIOR FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 438

LENGTH: 145

TYPE: PRT

ORGANISM: Homo sapiens

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

US-09-461-325-437

US-09-461-325-437

US-09-461-325-437

Query Match

Best Local Similarity 34.3%; Pred. NO. 3.7e-13;

Matches 49; Conservative 24; Mismatches 70; Indels 0; Gaps 0;

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

Sequence 438, Application US/10115123

Patent No. 6774216

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins

FILE REFERENCE: P2029630APID2

CURRENT APPLICATION NUMBER: US/10/115.123

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: PCT/US99/13418

PRIOR FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: 60/089,507

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,508

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,509

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,510

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/090,112

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090,113

PRIOR FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 438

LENGTH: 145

TYPE: PRT

ORGANISM: Homo sapiens

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

US-09-461-325-437

US-09-461-325-437

US-09-461-325-437

Query Match

Best Local Similarity 34.3%; Pred. NO. 3.7e-13;

Matches 49; Conservative 24; Mismatches 70; Indels 0; Gaps 0;

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

Sequence 438, Application US/10115123

Patent No. 6774216

GENERAL INFORMATION:

APPLICANT: Ruben et al.

TITLE OF INVENTION: 94 Human Secreted Proteins

FILE REFERENCE: P2029630APID2

CURRENT APPLICATION NUMBER: US/10/115.123

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: PCT/US99/13418

PRIOR FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: 60/089,507

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,508

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,509

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089,510

PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/090,112

PRIOR FILING DATE: 1998-06-22

PRIOR APPLICATION NUMBER: 60/090,113

PRIOR FILING DATE: 1998-06-22

NUMBER OF SEQ ID NOS: 532

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 438

LENGTH: 145

TYPE: PRT

ORGANISM: Homo sapiens

US-10-115-123-438

US-10-115-123-438

US-10-115-123-438

US-09-461-325-437

US-09-461-325-437

US-09-461-325-437

Query Match

Best Local Similarity 34.3%; Pred. NO. 3.7e-13;

Matches 49; Conservative 24; Mismatches 70; Indels 0;

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: Sequence 437, Application US/09461325A
: Patent No. 6475753
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: 94 Human Secreted Proteins
: FILE REFERENCE: P2029p1
: CURRENT APPLICATION NUMBER: US/09/461,325A
: CURRENT FILING DATE: 1999-12-14
: EARLIER APPLICATION NUMBER: FCT/US99/13418
: EARLIER FILING DATE: 1999-06-15
: EARLIER APPLICATION NUMBER: 60/089,507
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,508
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,509
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/089,510
: EARLIER FILING DATE: 1998-06-16
: EARLIER APPLICATION NUMBER: 60/090,112
: EARLIER FILING DATE: 1998-06-22
: EARLIER APPLICATION NUMBER: 60/090,113
: EARLIER FILING DATE: 1998-06-22
: NUMBER OF SEQ ID NOS: 532
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 437
: LENGTH: 308
: TYPE: PRT
: ORGANISM: Homo sapiens
: JS-09-461-325-437

```

Query Match	6.7%	Score 142;	DB 4;	Length 308;
Best Local Similarity	25.0%	Pred. No. 2.4e-06;		
Matches	47;	Conservative 32;	Mismatches 71;	Indels 38; Gaps 7;

Db	252	AISSSLAHP--QGIKSTGYHSAVLPFGVAVDTSCHLIPSPWLPVTLGVAGLISVNGA	309
Qy	91	AYLGNIQCIPAKKGLDMVHIGNMTLAGVAVGTAEMLMPLDYGALLIGFGIISTLIGF	150
Db	310	KYL-----RQCC--NRVLGIPHSISNGVNSLGLLEETIYYLLVDLYGAGNG	357
Qy	151	VYLPFPESRLHIQDTGCGINMLHGIP-----GIIGGVAVGTAAASASILEVVGK-EG	200
Db	358	MI-----GF-----QVLSIGELSLAVIALTSGLTALLNLNKIRAPHPAKYFD	403
Qy	201	LHSPFDQGFNGMDTARQGRFQIYGLLVTTAMALMGIIYGLILRLFPFGQSPDENCPE	260
Db	404	DOVEWKEP 411	
Qy	261	DAVYWEWP 268	

RESULT 8	
US-10-012-542-437	
/ Sequence 437, Application US/10012542	
/ Patent No. 6627741	
/ GENERAL INFORMATION:	
APPLICANT: Ruben et al.	
TITLE OF INVENTION: 94 Human Secreted Proteins	
FILE REFERENCE: P2029P1	
CURRENT APPLICATION NUMBER: US/10/012,542	
CURRENT FILING DATE: 2001-12-12	
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325	
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14	
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507	
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16	
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508	
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16	
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509	
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16	
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510	
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16	
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112	
PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22	

```

? PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
? PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
? NUMBER OF SEQ ID NOS: 532
? SOFTWARE: PatentIn Ver. 2.0
? SEQ ID NO 437
? LENGTH: 308
? TYPE: PRT
? ORGANISM: Homo sapiens
US-10-012-542-437

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Query Match 6.7%; Score 142; DB 4; Length 308;
Best Local Similarity 25.0%; Pred. No. 2.4e-06;
Matches 47; Conservative 32; Mismatches 71; Indels 38; Gaps 7,

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QY 252 ALSGSSLAHP---QGIKSTKYGSAVLPEGVAVDTSSCHLISPMPLPYLVAGIISVRGA 309
Db 91 AYLGGNIQCPAKKGLDMVHITONATLGAAGVAVGTAAEMMLPYGALITGVCGIISTLGF 150
QY 310 KYL-----PGCC--NRVLGIPIHSSINGVNFSLGLLEBIITYVLVLDTVPAANG 357
Db 151 VYLTPELSRLHIQPTCGNNLHGPR-----GIIGIVAVAVTAAASASLEVYCK-ES 200
QY 358 MI-----GF-----QVLISIGEELAIIVALTSGLLTALLINIKIRAPHEAKYRP 403
Db 201 LVHSFDQGFQNDMTARTQGRFQIYGLLVLTAMALMGIIYGLIRLPFWGQSDENCEE 260
QY 404 DQYFWKEP 411
Db 261 DAYVWEMP 268

```

```

RESULT 9
US-10-115-123-437
; Sequence 437, Application US/10115123
; Patent No. 6774216
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P202930APD2
; CURRENT APPLICATION NUMBER: US/10/115,123
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: PCT/US99/13418
; PRIOR FILING DATE: 1999-06-15
; PRIOR APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 437
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-115-123-437

```

```

Query Match      6.7%  Score 142, DB 4, Length 308;
Best Local Similarity 25.0%, Pred. No. 2,4e-06;
Matches 47, Conservative 32, Mismatches 71, Indels 38, Gaps 7

QY      252 AISGSSLAHP---OGKITSKTYGSAVLDEGVAVDTSCHLIDPSPMPLPVLGVAGLISVRGA 309
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      91 AILGNIQCFAKKGKGLDMVHILQNKLTLAGVAAGTAAEMMLMPGALLIGVCGIITLGF 150
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      310 KYL-----PQCC--NRVLGI PHSISGYNFSLGLLEBIIYIVLLVLDTVGANG 357
      :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Db      151 VYLTPLESRLHIDTGCINNLMGIP-----GIIGGIVGAVTAASALEYVGK-EG 200
Qy      358 MI-----GF-----QVLLSIGELSLAIVLITSGLLTALLNLRKRAPEHAYPD 403
Db      201 LVHSFDFQGRNGDWMTARTQGRFQYGLLVLTLMALMGITVGLTLRLPFGQSPDENCE 260
Qy      404 DOVFWKFP 411
Db      261 DAVYWEWP 268

RESULT 10
US-09-248-796A-20407
; Sequence 20407, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 20407
; LENGTH: 633
; TYPE: PR1
; ORGANISM: Candida albicans
US-09-248-796A-20407

Query Match      5.5%; Score 117.5; DB 4; Length 633;
Best Local Similarity 22.1%; Pred. No. 0.0027;
Matches 92; Conservative 69; Mismatches 142; Indels 113; Gaps 22;

Qy      5 YPSVORCLPLCATLEAAILLFFPTHVDASLEDDKGLVASYQVGODLTVMMAIGLGF 64
Db      83 YLNGVQ--LILCFSL--FLCLFLFAL-----DQTIYV-----TILTVGTRF 121
Qy      65 LTSSFRRHSSVAFNLFM-----LALGVOMAILLDGFLSQFPGSKVITLF-- 111
Db      122 --DAFSKVGMLSSGFLTMAVFIOFGKLSIIIRKAMV-----IAILFEA 167
Qy      112 -SIWLAWSLSTVLS--VDAVLGKNLAQLVNVLVEVDLGNLRVNSINFTDVM- 167
Db      168 GSLMCAIANDMNVLIIGRVLAGIGSGINSLVFVIGSEVVPITRRPLALS-IFSITPAVA 226
Qy      168 NMHHIYVFAAYFG-LTVAMCLPKPLPGTEEDNDQRATIPSLSAMLGLFLMPPRSVNSA 226
Db      227 SVVGPLIGGAFSTKVTYRMAFYINLPFG-----GPAITVLYAFPPRPKV 272
Qy      227 LRSPIERKNAVNTYVAVAVSVTAISGSLAHPOCKISKTYGHSANLDEGVAVDTSCH 286
Db      273 NVKQQLKQFD-YFGTFLLIGSVILL-----LAITFETSD-FPMDSAAVISC- 317
Qy      287 LTPSPMLPIYLG--LVAGLSVRGAKYLRGCCNRVLGIPHSIMGNSFSLGLEERTIY 343
Db      318 -----FVLGPLYLLIAFVVMNGFSPKNOVISTEIVKP--QIIASTLAISGIFSAFIM 367
Qy      344 IYLLVLDTVGAGNMGIGFOYL-----LSIGELSLAIVLITSGLLTALLNLRKIRK 394
Db      368 FMYY-----GATFYQVVKDASPLSAGLHLPTIIAV---VLSMGLSLVQK 411

RESULT 11
US-09-710-279-2020
; Sequence 2020, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
```

```
; FILE REFERENCE: PUJ3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2020
; LENGTH: 801
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-2020

Query Match      5.4%; Score 114; DB 4; Length 801;
Best Local Similarity 20.9%; Pred. No. 0.009;
Matches 103; Conservative 79; Mismatches 172; Indels 138; Gaps 23;

Qy      9 VQRCLPLCA-----LTLEAAILLFFPTHYDASL-----EDCKGLVASYQVGODLT 55
Db      259 IARTPIFAISEGWMTITL-VGLITLFW-----ASLNRKQHDGLLAFSTVSQGM 311
Qy      56 VMAAIGL-----GFLTSSFRRHSSWSVAFNLFMLAGVQMAI----- 92
Db      312 IMSWLGIGAVSYHYOGANSQLYVAGFYAAIFHLINHAIFKALFMITGIDHSGTRDVK 371
Qy      93 LLDGFLSQFPGSKVITLFSIWLATMSALSVDVAVL-GKNLAQLVNVLVEVDLGN 151
Db      372 KLGGELTIMPISFTLVITTLMSAGVPPFNGFLSKERFLSMMIVTTLNLSLTLGLILL 431
Qy      152 NLRNVISINFTDTHNM-NMHHIYVFAAYFGITVAMCLPKPLPGTEEDNDQRATIPSLSAM 210
Db      432 PIIAIIISITFYYSIKFIHLIF-FGSY-----KPAIPKAAHSSILMLISPIILT 482
Qy      211 LGALFLMPPRSVNSALLRSPIERKN-----AVFTYVAVA-----VSV 249
Db      483 SLIVIRGLF-PSI---LTGSLIEPASVAVSQTNSITHEFHLPHDITAPLSTIGIYIIGI 538
Qy      250 VTAISGS-----SLAH-OGKISKTYGHSANLDEGVAVDTSCHLIPS----- 290
Db      539 LLIIISFSYWRLLQAHFYQLTLNHWY-----DTSGQRIPGYSSENITNSVYTG 586
Qy      291 --PWLPIVLGVLAVGLISVRGAKYLRGCCNRVLGIPHSISNGVNSLGLLEIITYULV 348
Db      587 SRNNLVIIILILALTFV-----TVISVP-SIDPKVNSHURVEGATVLELLI 634
Qy      349 LDT--VGAGNGMIGFOYLSIGEL-----SLAIVLITSGLLTALLNLRKIRKA 395
Db      635 ASTFIIRAKSRLPSTIMLSAVGVAISVLFIFKAPDIALQFVVESTALFL-LCFYHL 693
Qy      396 PHEAKYFDDQVF 407
Db      694 PNLNRVNEKPTF 705

RESULT 12
US-09-134-001C-3105
; Sequence 3105, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
```

SEQ ID NO 3105
 LENGTH: 808
 TYPE: PRF
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3105

Query Match 5.4%; Score 114; DB 3; Length 808;
 Best Local Similarity 20.9%; Pred. No. 0.0091; Indels 138; Gaps 23;
 Matches 103; Conservative 79; Mismatches 172;

```

QY 9 VORCEPLCA-----LTLEALLILFFFTHYDASL-----EDOKGLVASYQVQDIL 55
DB 266 IARITIFPAISEGWWTITL-VGLITLFW-----ASINATKHQDLKGLAFSTVQLGM 318
QY 56 VMAAIGL-----GFLTSSFRHSSVAFNLPMIALGVQMAI----- 92
DB 319 IMSMLGIGAVSYHYOGANSQLVYAGFVAALFHLINHTPEKALFMTGTGIDHSTGRDYK 378
QY 93 LLDGFLSQPPSGKVVITLPSIMLATMSALSVLSVDAVL-GKVNLAQLVVMVLEVTDLG 151
DB 379 KLGGLLTMFTISTLTLYITLTSWAGVPPENGFLSKKEFLSMINVTHTLMSINTGLL 438
QY 152 NLRMVISNIFNTDYHNN-MMHIVFAAFGLTVAMCLPKPLPEGTEDNDQRAITPSLSAM 210
DB 439 PIAIIGSITFYYSIKFILHIF-FGSY-----KPEALPKOAHSSITLMLISPIILT 489
QY 211 LGLFLMFRPSVNSALRSPIERKA-----AVFTTYAVA-----VSV 249
DB 490 SLVIVFGLF-PSI---LTOSIEPASVAVSQTNTAEFHLFPHGIPPAFLSTIGIYIGI 545
QY 250 VTMAISGS-----SLAHP-OGKISKTYGSAVLPEGVAVDTPSCHLIPB----- 290
DB 546 LLIISSYVWRLLOAHRYQLTLNHWY-----DTSGRIRIPYSNINTNSYVTGF 593
QY 291 --PMLPIVLGLVAGLISVRGAKYLPGCCNRVLGPHSSINGVNSLGLIEITIVYLLV 348
DB 594 SRNNLVITLIGLITLALFEV-----TVISVVF-SIDPKVSHLRVEGATVLFLLI 641
QY 349 LDT--VAGNGMIGFOVLISIGEL-----SLAIYALTSGLLTALLNLKIRKA 395
DB 642 ASFTFIIFAKRLPSIIMLSAVGVAISVLFEPKAPDIALQFVESISTALFL-LCYHL 700
QY 396 PHEAKYFDDQVF 407
DB 701 PNLARNYKEPTF 712

```

RESULT 13

US-09-489-039A-7527
 Sequence 7527, Application US/09489039A
 Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709,2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 7527
 LENGTH: 447
 TYPE: PRF
 ORGANISM: Klebsiella pneumoniae
 US-09-489-039A-7527

Query Match 5.3%; Score 113.5; DB 4; Length 447;
 Best Local Similarity 22.7%; Pred. No. 0.0042;
 Matches 85; Conservative 51; Mismatches 118; Indels 121; Gaps 17;
 QY 56 VMAAIGLGTSSFRHSSVAFNLPMIALGVQMAIILDDFLSQPPSGKVVITLPSLWL 115

```

DB 157 VMAIGLNLAPIAIV--SVSASAFDSMMAVL-----TVLCIGIVAVFTRGMLQRLIILVGL 210
QY 116 ATMSALSTLISVDNLGK-----VNL AOLV-----VMVLVEVTD 149
DB 211 IVACALYALDLANGLGLGKPLDPSPLAQAAPGLPHFTTPSPRGAMMLIAPAVILVAEN 270
QY 150 LGNLRMVISNIFNTDYHNNMMHIVFAAFGLTVAMCLPKPLPEGTEDNDQRAITPSLSA 209
DB 271 LGHLKAAVAGMGRN-----MDPYGRAFPVG-----DGLATM--LSG 304
QY 210 MGALFLMFRPSVNSALRSPIERKAVENTTYAVAVSVTAISGSSLAHQKISIKTY 269
DB 305 SVGSGGVTTYAENIG-----VMAVTKYSTLVEVAALLIAMLIG-----FSPKF 348
QY 270 GHSVVLPEGVAVDTSCHLIPSPMLPIVLG-----LVAGLISVGAKYLPGCCNRVLGIPHS 325
DB 349 G-----ALHTITPGP---VIGGASIVFGILAVAGAR-----IMVQNR 383
QY 326 SIMGVNFSLLGLEEITIVILLVDTVGANGMIGFOVLISIGELSLAIVALTGGLTA 385
DB 384 VDLSONSLN-----IMSVTLVL--GAGD-----FALSIGFTLGGITGATRG--A 425
QY 386 LLNLKIRKAPHEAK 400
DB 426 ILLHALLHRTREAK 440

```

RESULT 14

US-09-134-001C-5655
 Sequence 5655, Application US/09134001C
 Patent No. 6380370
 GENERAL INFORMATION:
 APPLICANT: Lynn Doucelte-Stamm et al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC-007
 CURRENT APPLICATION NUMBER: US/09/134,001C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/064,964
 PRIOR FILING DATE: 1997-11-08
 PRIOR APPLICATION NUMBER: US 60/055,779
 PRIOR FILING DATE: 1997-08-14
 NUMBER OF SEQ ID NOS: 5674
 SEQ ID NO 5655
 LENGTH: 800
 TYPE: PRF
 ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-5655

Query Match 5.2%; Score 110; DB 3; Length 800;
 Best Local Similarity 19.2%; Pred. No. 0.024;
 Matches 98; Conservative 74; Mismatches 150; Indels 188; Gaps 21;

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QY 17 ALTLLEAALLILFFY-----FTHYDASLE-----DOKGLVASYQVQD 52
DB 250 ATWAKGIFLFFFTPLGLSNVYITVTFVGLITMLFGSLTLRQYDLKGLIAYTISQ 309
QY 53 DLTWMAAIGLGTSSFRHSSVAFNLPMIALGVQMAI-----FNL-----FMALAI----- 86
DB 310 LGNIMTMVGLG---GGYAOHTSDELSKFTYLLVFAGLFHLMMNNAFKCALFMVGIIIDHE 366
QY 87 -GVQWAILLDGFLSQPPSGKVVITLPSIMLATMSALSVLSVDAVLGKVNLAQ----- 138
DB 367 SGTREDIRLLNGMKRVKPKMIIWMLLAALSWAGVPLNGFLSKMPLDSLTKANELDQYGF 426
QY 139 LVVMVLEVETDGLNLRMVISNIFNTDYHNNMMHIVFAAFGLTVAMCLPKPLPEGTEDN 198
DB 427 VLFVVIISIG-----VLSILTFYALYMIKETFWGNV---NIEKFKKQIHEP----- 472
QY 199 DORATTPSISAMUGALFLMWR-PSVNSALRSPIERKAVENTTYAV-----AVSVTAL 253
DB 473 -----WLFSLPAVILMLLIVIFVFPVFNQFVILPATRSVSGIGAE 514

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 24, 2005, 13:13:48 ; Search time 19 Seconds
(without alignments)
2111.705 Million cell updates/sec

Title: CAC07879

Sequence: 1 MSCKYPRSVRCPLCALTL.....EAKYDDQVFWKPHLAVGF 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR.79:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1981	93.3	417	2	152615 gene Rhd protein -
2	1976	93.0	417	2	A46368 erythrocyte membra
3	1863	87.7	417	2	I37005 Rhesus-like protei
4	1842	86.7	417	2	I37076 Rhesus-like protei
5	1840	86.6	417	2	I37004 Rhesus-like protei
6	1833	86.3	417	2	A30405 erythrocyte membra
7	1811	85.3	417	2	I37003 Rhesus-like protei
8	1803	84.9	417	2	I37075 Rhesus-like protei
9	1509	76.1	417	2	I84434 Rhesus blood group
10	1411	66.4	354	2	S78480 Rhesus blood group
11	1294	60.9	354	2	I37053 Rhesus blood group
12	1089.5	51.3	265	2	S78479 Rhesus blood group
13	1000.5	47.1	267	2	S78478 Rhesus blood group
14	547.5	25.8	409	2	S29124 membrane glycoprot
15	412	19.4	463	2	T29442 hypothetical prote
16	361.5	17.0	457	2	T18673 hypothetical prote
17	161	7.6	44	2	PC2033 RbPI-beta polypept
18	128	6.0	475	2	T01260 probable ammonium
19	127	6.0	458	2	C82232 proton/glutamate s
20	126	5.9	421	2	B84129 ammonium transport
21	125.5	5.9	468	2	A69468 ammonium transport
22	120	5.6	537	1	F70705 hypothetical prote
23	119.5	5.6	388	2	C64722 Na+/H+-exchanging
24	119.5	5.6	394	2	AH0362 nucleoside permeas
25	119.5	5.6	424	2	B69172 cationic amino aci
26	119.5	5.6	891	2	B82495 probable NADH dehy
27	119	5.6	881	2	S46633 RbPI-alpha polypep
28	118	5.6	42	2	PC2032 Na+/H antiporter
29	117.5	5.5	388	2	A99631

30	117.5	5.5	388	2	A85482 Na+/H antiporter,
31	117.5	5.5	612	2	G64678 NADH2 dehydrogenas
32	114.5	5.4	481	2	C87435 conserved hypothec
33	114	5.4	800	2	G89831 hypothetical prote
34	113.5	5.3	333	2	E96954 Na/H antiporter (n
35	113	5.3	653	2	D82352 Iron(III) ABC tran
36	113	5.3	685	2	AC0527 ferriochrome transp
37	113	5.3	782	2	T25925 hypothetical prote
38	112.5	5.3	419	2	D64142 hypothetical prote
39	112	5.3	385	2	G82789 permease Xf0589 (1
40	111.5	5.2	437	2	JC4988 high-affinity gluc
41	111.5	5.2	449	2	H69423 branched-chain ami
42	111	5.2	660	2	A64739 ferriochrome-iron t
43	110.5	5.2	438	2	AD0481 probable gluconate
44	110.5	5.2	448	2	E97907 phosphotransferase
45	110.5	5.2	612	2	E71839 NADH2 dehydrogenas

ALIGNMENTS

RESULT 1

152615
gene Rhd protein - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence #revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: 152615
R: Huang, C.H.; Reid, M.E.; Chen, Y.
Blood 86, 784-790, 1995
A:Title: Identification of a partial internal deletion in the RH locus causing the human
A:Reference number: 152615; MUID:95329738; PMID:7606008
A:Accession: 152615
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-417 <RBS>
A:Cross-references: UNIPROT:Q02161; GB:S78509; NID:G999309; PID: AAB34852.1; PID:G999310
C:Genetics:
A:Gene: Rhd
C:Superfamily: human erythrocyte membrane protein Rhd

Query Match	93.3%	Score 1981	DB 2	Length 417
Best Local Similarity	95.0%	Pred. No. 1.2e-150		
Matches	396	Conservative	4	Mismatches 17; Indels 0; Gaps 0;
QY	1	MSCKYPRSVRCPLCALTLTEAALLLPFFTHYDASLEDOQKIVASYOGQDLTWAAI	60	
DB	1	MSCKYPRSVRCPLCALTLTEAALLLPFFTHYDASLEDOQKIVASYOGQDLTWAAI	60	
QY	61	GLGFLTSSFRHSSVAFNLFMLALGVQWAILLDGFLSQPPSGKVITLPSIWLATMSA	120	
DB	61	GLGFLTSSFRHSSVAFNLFMLALGVQWAILLDGFLSQPPSGKVITLPSIWLATMSA	120	
QY	121	LSVLISVDAILGKNVLAQLVVMVLVEVTDLGNLRMVISNIFNTDYHNMWHIYVFAA	180	
DB	121	LSVLISVDAILGKNVLAQLVVMVLVEVTDLGNLRMVISNIFNTDYHNMWHIYVFAA	180	
QY	181	LTYAWCLPKPLPGSTENDQRTIPSLAMLGALFLMFPSPVNSALLBSPTEKNAVEN	240	
DB	181	LSVAMCLPKPLPGSTENDQRTIPSLAMLGALFLMFPSPVNSALLBSPTEKNAVEN	240	
QY	241	TYVAVAVSVTALISGSSLAHPQGIKSTYGHSAVLPGGVAVDTPSCHLIPSPWLPIVGLV	300	
DB	241	TYVAVAVSVTALISGSSLAHPQGIKSTYGHSAVLPGGVAVDTPSCHLIPSPWLPIVGLV	300	
QY	301	AGLISVGAKYLPQCCNRVLGIPHSISMGYNFSLGLLEBIYIVLVLDVTGAGNGMIG	360	
DB	301	AGLISVGAKYLPQCCNRVLGIPHSISMGYNFSLGLLEBIYIVLVLDVTGAGNGMIG	360	
QY	361	FQYVLISGELSLAIVALTSGLLTALLLNKIKKAPBEAVFPDQVFWKPHLAVGF	417	
DB	361	FQYVLISGELSLAIVALTSGLLTALLLNKIKKAPBEAVFPDQVFWKPHLAVGF	417	

RESULT 2
A46368
erythrocyte membrane protein Rhd - human
N:Alternate names: blood group antigen Rn(D)
C:Species: Homo sapiens (man)
C>Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A:Accession: A46368; S26564; S26561; I52581; S02085; S02087; A32509; A30216; A61174; I52
R:Le van Kim, C.; Mourou, I.; Cherif-Zahar, B.; Raynal, V.; Cherrier, C.; Cartton, J.P.;
Proc. Natl. Acad. Sci. U.S.A. 89, 10925-10929, 1992
A>Title: Molecular cloning and primary structure of the human blood group Rhd polypeptide
A:Reference number: A46368; MUID:9306356; PMID:1438298
A:Accession: A46368
A:Molecule type: mRNA
A:Residues: 1-417 <LEV2>
A:Cross-references: UNIPROT:Q02161; GB:X63097; GB:S48953; NID:936046; PIDN:CAA44811.1; F
A:Experimental source: bone marrow, clone RnXIII
A>Note: sequence extracted from NCBI backbone (NCBIN:118725, NCBID:118726)
R:Le van Kim, C.; Cherif-Zahar, B.; Raynal, V.; Mourou, I.; Lopez, M.; Cartton, J.P.; Col
Blood 80, 1074-1078, 1992
A>Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing.
A:Reference number: S26560; MUID:92360855; PMID:1379850
A:Accession: S26564
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-417 <LEV2>
A:Cross-references: EMBL:X63097; GB:S48953; NID:936046; PIDN:CAA44811.1; PID:936047
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
A:Accession: S26561
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-217 'M', 219-417 <LEV3>
A:Cross-references: EMBL:X63094; NID:936027; PIDN:CAA44808.1; PID:936028
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
R:Arce, M.A.; Thompson, E.S.; Wagner, S.; Coyne, K.E.; Ferdman, B.A.; Lublin, D.M.
Blood 82, 651-655, 1993
A>Title: Molecular cloning of Rhd cDNA derived from a gene present in Rhd-positive, but
A:Reference number: I52581; MUID:93320449; PMID:8329718
A:Accession: I52581
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-217 'M', 219-417 <RES>
A:Cross-references: GB:I08429; NID:9337390; PIDN:AA02679.1; PID:9337391
R:Avent, N.D.; Ridgwell, K.; Mabry, W.J.; Tanner, M.J.A.; Ametee, D.J.; Kumpel, B.
Biochem. J. 256, 1043-1046, 1988
A>Title: Protein-sequence studies on Rh-related polypeptides suggest the presence of at
A:Reference number: S02085; MUID:89134163; PMID:3146980
A:Accession: S02085
A:Molecule type: protein
A:Residues: 2-11, 'X', 13-33 <AVE1>
A>Note: this peptide was designated blood group Rh-related protein D30
A:Accession: S02087
A:Molecule type: protein
A:Residues: 2-11, 'X', 13-14 <AVE2>
R:Blouy, C.; Blanchard, D.; Dahr, W.; Beyreuther, K.; Salmon, C.; Cartton, J.P.
Blood 72, 661-666, 1988
A>Title: Determination of the N-terminal sequence of human red cell Rn(D) polypeptide an
A:Reference number: A32509; MUID:88294325; PMID:3135863
A:Accession: A32509
A:Molecule type: protein
A:Residues: 2-11, 'L', 13-15, 'X', 17 <BLD>
R:Saboort, A.M.; Smith, B.L.; Agre, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 4042-4045, 1988
A>Title: Polymorphism in the M-r 32,000 Rh protein purified from Rh(D)-positive and -neg
A:Reference number: A30216; MUID:88234555; PMID:3131772
A:Accession: A30216
A:Molecule type: protein
A:Residues: 2-11, 'X', 13-21 <SAB>
R:Suyama, K.; Goldstein, J.; Abersold, R.; Kent, S.
Blood 77, 411, 1991
A>Title: Regarding the size of Rh proteins.
A:Reference number: A61174; MUID:91091537; PMID:1898705
A:Accession: A61174

A:Molecule type: protein
A:Residues: 401-407, 'DI' <SU7>
R:Westhoff, C.M.; Wylie, D.E.
Blood 83, 3098-3100, 1994
A>Title: Identification of a new Rhd-specific mRNA from K562 cells.
A:Reference number: I52589; MUID:94235883; PMID:8180407
A:Accession: I52589
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-217 'M', 219-313, 410-417 <RE2>
A:Cross-references: GB:S70174; NID:9546725; PIDN:AAB30756.1; PID:9546726
R:Suyama, K.; Lunn, R.; Haller, S.; Goldstein, J.
Blood 84, 1975-1981, 1994
A>Title: Rn(D) antigen expression and isolation of a new Rh(D) cDNA isoform in human ery
A:Reference number: I52596; MUID:94362249; PMID:8080999
A:Accession: I52596
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-217 'M', 219-313, 'V', 315, 'S' <RE3>
A:Cross-references: GB:S73913; NID:9693866; PIDN:AAB31911.1; PID:9693867
C:Genetics:
A:Gene: GDB:RHD; RH; RHD
A:Cross-references: GDB:119551; OMIM:111680
A:Map position: 1p36.2-1p34
C:Superfamily: human erythrocyte membrane protein Rhd
C:Keywords: erythrocyte; surface antigen; transmembrane protein

Query Match 93.0%; Score 1976; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 36-150;
Matches 396; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSCKYRSVORCLP/CATLREANLILPFYFTHYDASLEDQGLVASYQVGDLTWMAI 60
DB 1 MSCKYRSVORCLP/MALTLREALILFFPHYDASLEDQGLVASYQVGDLTWMAI 60
QY 61 GLGFLTSPFRHSWSVAFNLFMALGVQWAILLDGFLSOPFSKAVITLPSIMLATMSA 120
DB 61 GLGFLTSPFRHSWSVAFNLFMALGVQWAILLDGFLSOPFSKAVITLPSIMLATMSA 120
QY 121 LSVLISVDVAVLGNLAQIVWVWVLEVDLGNLRVNSINFTVDYHMMMHIIYPAAYFG 180
DB 121 LSVLISVDVAVLGNLAQIVWVWVLEVDLGNLRVNSINFTVDYHMMMHIIYPAAYFG 180
QY 121 LSVLISVDVAVLGNLAQIVWVWVLEVDLGNLRVNSINFTVDYHMMMHIIYPAAYFG 180
DB 121 LSVLISVDVAVLGNLAQIVWVWVLEVDLGNLRVNSINFTVDYHMMMHIIYPAAYFG 180
QY 181 LTVANCLPKPLPEGEENDORATIPSLSAMGALFIMFRSVNSALLRSIERKNVFN 240
DB 181 LTVANCLPKPLPEGEENDORATIPSLSAMGALFIMFRSVNSALLRSIERKNVFN 240
QY 241 TYAAVAVSVTAISGSSIAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPVLGLV 300
DB 241 TYAAVAVSVTAISGSSIAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPVLGLV 300
QY 301 AGLISVRGAKYLPGCCNNVLGIPIHSSIMGNFSLGLLEIITVVLVDVAGNMGIG 360
DB 301 AGLISVRGAKYLPGCCNNVLGIPIHSSIMGNFSLGLLEIITVVLVDVAGNMGIG 360
QY 361 FOVLISIGELSLAIVALTSGLTALTALNLTIRKAPAEAKYFDQVWPKPFLAVGF 417
DB 361 FOVLISIGELSLAIVALTSGLTALTALNLTIRKAPAEAKYFDQVWPKPFLAVGF 417

RESULT 3
I37005
Rhesus-like protein - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
R:Salvirol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie,
Biochem. Genet. 32, 201-221, 1994
A>Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the f
A:Reference number: I37003; MUID:95085595; PMID:7993375
A:Accession: I37005
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA

A;Residues: 1-417 <RES>
A;Cross-references: UNIPROT:Q28814; GB:L37053; NID:G606991; PID:AAA65624.1; PID:G606992
C;Superfamily: human erythrocyte membrane protein Rhd

Query Match 87.7%; Score 1863; DB 2; Length 417;
Best Local Similarity 89.2%; Pred. No. 3,2e-141;
Matches 372; Conservative 12; Mismatches 33; Indels 0; Gaps 0;

QY 1 MSCKYPSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60
DB 1 MSCKYPSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60
QY 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPSGKVITLFSIRLATMSA 120
DB 61 GFGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPSGKVITLFSIRLATMSA 120
QY 121 LSVLISVDALVAGKVNLAQLVVMVLVEYTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180
DB 121 LSVLISVDALVAGKVNLAQLVVMVLVEYTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDQATIPSLSAMIGALFLMFRPSVNSALRSPIERKNAVF 240
DB 181 LTVAMCLPKPLPKGTEDNDQATIPSLSAMIGALFLMFRPSVNSALRSPIERKNAVF 240
QY 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPGVAVDTSCHLIPSPWLPIYGLV 300
DB 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPGVAVDTSCHLIPSPWLPIYGLV 300
QY 301 AGLISVGAKYLPCCNCRVLGIPHSIMGVNFSLLGLEELIYVLLVDTVGAGNMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSIMGVNFSLLGLEELIYVLLVDTVGAGNMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPEHLAVGF 417
DB 361 FOVLIRIGESLATTIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPEHLAVGF 417

RESULT 4
137076
Rhesus-like protein - gorilla
C;Species: Gorilla gorilla (gorilla)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Accession: I37076
R;Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994
A;Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A;Reference number: I37003; MUID:95085595; PMID:7993375
A;Accession: I37076
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-417 <RES>
A;Cross-references: UNIPROT:Q28427; GB:L37053; NID:G607011; PID:AAA65627.1; PID:G607012
C;Superfamily: human erythrocyte membrane protein Rhd

Query Match 86.7%; Score 1842; DB 2; Length 417;
Best Local Similarity 89.0%; Pred. No. 1.5e-139;
Matches 371; Conservative 11; Mismatches 35; Indels 0; Gaps 0;

QY 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPGVAVDTSCHLIPSPWLPIYGLV 300
DB 241 TYVAVAVSVTVAISVSSLAHPQGIKSTYGHSAVLPGVAVDTSCHLIPSPWLPIYGLV 300
QY 301 AGLISVGAKYLPCCNCRVLGIPHSIMGVNFSLLGLEELIYVLLVDTVGAGNMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSIMGVNFSLLGLEELIYVLLVDTVGAGNMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPEHLAVGF 417
DB 361 FOVLIRIGESLATTIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPEHLAVGF 417

RESULT 5
137004
Rhesus-like protein - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C;Accession: I37004
R;Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie, Biochem. Genet. 32, 201-221, 1994
A;Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the A;Reference number: I37003; MUID:95085595; PMID:7993375
A;Accession: I37004
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-417 <RES>
A;Cross-references: UNIPROT:Q28813; GB:L37049; NID:G606989; PID:AAA65623.1; PID:G606990
C;Superfamily: human erythrocyte membrane protein Rhd

Query Match 86.6%; Score 1840; DB 2; Length 417;
Best Local Similarity 88.7%; Pred. No. 2.2e-139;
Matches 370; Conservative 11; Mismatches 36; Indels 0; Gaps 0;

QY 1 MSCKYPSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60
DB 1 MSCKYPSVQRCLPLCALTEEAAILLFYFPTHYDASLEDDKGLVASVYQGDLTWAAI 60
QY 61 GLGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPSGKVITLFSIRLATMSA 120
DB 61 GFGFLTSSFRHSHSSVAFLFMLALGVQMAILLDGLSOPPSGKVITLFSIRLATMSA 120
QY 121 LSVLISVDALVAGKVNLAQLVVMVLVEYTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180
DB 121 LSVLISVDALVAGKVNLAQLVVMVLVEYTDLGNLRMVISNIFNTDYHNMNMHIYVFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDQATIPSLSAMIGALFLMFRPSVNSALRSPIERKNAVF 240
DB 181 LTVAMCLPKPLPKGTEDNDQATIPSLSAMIGALFLMFRPSVNSALRSPIERKNAVF 240
QY 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPGVAVDTSCHLIPSPWLPIYGLV 300
DB 241 TYVAVAVSVTVAISGSSLAHPQGIKSTYGHSAVLPGVAVDTSCHLIPSPWLPIYGLV 300
QY 301 AGLISVGAKYLPCCNCRVLGIPHSIMGVNFSLLGLEELIYVLLVDTVGAGNMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSIMGVNFSLLGLEELIYVLLVDTVGAGNMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPEHLAVGF 417
DB 361 FOVLIRIGESLATTIALTSGLLTALLNLKIRKAPHEAKYFDDQVFWKPEHLAVGF 417

RESULT 6
A30405
erythrocyte membrane protein Rh (unknown specificity) - human
N;Alternate names: blood group Rh antigen
C;Species: Homo sapiens (man)
C;Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 09-Jul-2004
C;Accession: A30405; S13060; I54273; S40515; S40517; S02085; S02087; A32509; A307; R;Cherif-Zahar, B.; Bloy, C.; Le Van Kim, C.; Blanchard, D.; Bailly, P.; Hermand, P.; Sai Proc. Natl. Acad. Sci. U.S.A. 87, 6243-6247, 1990

A:Title: Molecular cloning and protein structure of a human blood group Rh polypeptide.
 A:Reference number: A30405; MUID:90349591; PMID:1696722
 A:Accession: A30405
 A:Molecule type: mRNA
 A:Residues: 1-417 <CHR>
 A:Cross-references: UNIPROT:P18577; GB:M34015; NID:G337398; PIDN:AAA36567.1; PID:G337398
 R:Avant, N.D.; Ridgwell, K.; Tanner, M.J.A.; Anstee, D.J.
 Biochem. J. 271, 821-825, 1990
 A:Title: cDNA cloning of a 30 kDa erythrocyte membrane protein associated with Rh (Rhesu
 A:Reference number: S13060; MUID:91058522; PMID:2123099
 A:Accession: S13060
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-417 <EMB>
 A:Cross-references: EMBL:X54534; NID:G36017; PIDN:CAA38401.1; PID:G36018
 R:Kajli, E.; Umenishi, F.; Iwamoto, S.; Ikemoto, S.
 Hum. Genet. 91, 157-162, 1993
 A:Title: Isolation of a new cDNA clone encoding an Rh polypeptide associated with the Rh
 A:Reference number: I54273; MUID:93216282; PMID:7916743
 A:Accession: I54273
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-417 <RES>
 A:Cross-references: GB:S57967; NID:G299049; PIDN:AAE26080.1; PID:G299050
 R:Mouto, I.; Collin, Y.; Cherif-Zahar, B.; Cartrom, J.P.; Le van Kim, C.
 Nature Genet. 5, 62-65, 1993
 A:Title: Molecular genetic basis of the human Rhesus blood group system.
 A:Reference number: S40515; MUID:94035121; PMID:2220426
 A:Accession: S40515
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1301,'F',303-417 <MOU1>
 A:Accession: S40516
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-225,'A',227-301,'F',303-417 <MOU2>
 A:Accession: S40517
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15,'C',17-59,'I',61-67,'S',69-102,'S',104-225,'A',227-301,'F',303-417 <MO3
 R:Avant, N.D.; Ridgwell, K.; Mawby, W.J.; Tanner, M.J.A.; Anstee, D.J.; Kumpel, B.
 Biochem. J. 256, 1043-1046, 1988
 A:Title: Protein-sequence studies on Rh-related polypeptides suggest the presence of at
 A:Reference number: S02085; MUID:89134163; PMID:3146980
 A:Accession: S02085
 A:Molecule type: protein
 A:Residues: 2-11,'X',13-33 <AVE2>
 A:Note: this peptide was designated blood group Rh-related protein D30
 A:Accession: S02087
 A:Molecule type: protein
 A:Residues: 2-11,'X',13-14 <AVE3>
 R:Bloly, C.; Blanchard, D.; Dahr, W.; Beyreuther, K.; Salmon, C.; Cartrom, J.P.
 Blood 72, 661-666, 1988
 A:Title: Determination of the N-terminal sequence of human red cell Rh(D) polypeptide an
 A:Reference number: A32509; MUID:88294325; PMID:3135863
 A:Accession: A32509
 A:Molecule type: protein
 A:Residues: 2-11,'L',13-15,'X',17 <BLO>
 R:Saboori, A.M.; Smith, B.L.; Agre, P.
 Proc. Natl. Acad. Sci. U.S.A. 85, 4042-4045, 1988
 A:Title: Polymorphism in the M-r 32,000 Rh protein purified from Rh(D)-positive and -neg
 A:Reference number: A30216; MUID:88234555; PMID:3131772
 A:Accession: A30216
 A:Molecule type: protein
 A:Residues: 2-11,'X',13-21 <SAB>
 R:Syama, K.; Goldstein, J.; Abersold, R.; Kent, S.
 Blood 77, 411, 1991
 A:Title: Regarding the size of Rh proteins.
 A:Accession: A61174; MUID:91091537; PMID:1698705
 A:Molecule type: protein
 A:Residues: 401-407, 'DI' <SUY>

C:Superfamily: human erythrocyte membrane protein Rhd
 C:Keywords: alternative splicing; erythrocyte; surface antigen; transmembrane protein

Query Match 86.3%; Score 1833; DB 2; Length 417;

Best Local Similarity 88.7%; Pred. No. 7.9e-139;

Matches 370; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

```

QY 1 MSCKYPSVORCLPLCALTEEAALLLFYFPTHYDASLEDOKGLVASYGVQODLTWMAI 60
DB 1 MSCKYPSVORCLPLCALTEEAALLLFYFPTHYDASLEDOKGLVASYGVQODLTWMAI 60
QY 61 GLGFLTSSFRHRHSSVAFMLFMALGVQWAILLDGFLSQFPFGKVVITLFSIRLATMSA 120
DB 61 GLGFLTSSFRHRHSSVAFMLFMALGVQWAILLDGFLSQFPFGKVVITLFSIRLATMSA 120
QY 121 LSVLISYDAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
DB 121 LSVLISYDAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
QY 121 MSVLISAGAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
DB 121 MSVLISAGAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
DB 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
QY 241 TTYAVAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
DB 241 TTYAVAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
QY 241 TTYALAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
DB 241 TTYALAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
QY 301 AGLSIVGAKYLPGCCNRYLGIPIHSGIMKYNFSLGLEELIYIVLVLDYTGAGNGMIG 360
DB 301 AGLSIVGAKYLPGCCNRYLGIPIHSGIMKYNFSLGLEELIYIVLVLDYTGAGNGMIG 360
QY 361 FOVLISIGLSLAIVALTSLGTLTLLNLTKRKAPHEAKYRDDDOYFKFPHLAVGF 417
DB 361 FOVLISIGLSLAIVALTSLGTLTLLNLTKRKAPHEAKYRDDDOYFKFPHLAVGF 417

```

RESULT 7

Rhesus-like protein - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C>Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004

C/Accession: I37003

R:Salvignon, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Collin, Y.; Ruffie, C.

Biochem. Genet. 32, 201-221, 1994

A:Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the f

A:Reference number: I37003; MUID:95085595; PMID:7993375

A:Accession: I37003

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-417 <RES>

A:Cross-references: UNIPROT:Q28812; GB:I37048; NID:9606987; PIDN:AAA65622.1; PID:9606988

C:superfamily: human erythrocyte membrane protein RHD

Query Match 85.3%; Score 1811; DB 2; Length 417;

Best Local Similarity 87.5%; Pred. No. 4.5e-137;

Matches 365; Conservative 11; Mismatches 41; Indels 0; Gaps 0;

```

QY 1 MSCKYPSVORCLPLCALTEEAALLLFYFPTHYDASLEDOKGLVASYGVQODLTWMAI 60
DB 1 MSCKYPSVORCLPLCALTEEAALLLFYFPTHYDASLEDOKGLVASYGVQODLTWMAI 60
QY 61 GLGFLTSSFRHRHSSVAFMLFMALGVQWAILLDGFLSQFPFGKVVITLFSIRLATMSA 120
DB 61 GLGFLTSSFRHRHSSVAFMLFMALGVQWAILLDGFLSQFPFGKVVITLFSIRLATMSA 120
QY 121 LSVLISYDAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
DB 121 LSVLISYDAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
QY 121 LSVLISAGAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
DB 121 LSVLISAGAVLGKVNLAQLVWMLVEVTDLGNLRMTVSNIFNTDYMNMNHIVFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
DB 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
QY 241 TTYAVAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
DB 241 TTYAVAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
QY 241 TTYALAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
DB 241 TTYALAVSVYTTAISGSLAHPOGKISKYGHSAVLPEGVAVDTSCHLTPSPWLPYVLGLV 300
QY 301 AGLSIVGAKYLPGCCNRYLGIPIHSGIMKYNFSLGLEELIYIVLVLDYTGAGNGMIG 360
DB 301 AGLSIVGAKYLPGCCNRYLGIPIHSGIMKYNFSLGLEELIYIVLVLDYTGAGNGMIG 360
QY 361 FOVLISIGLSLAIVALTSLGTLTLLNLTKRKAPHEAKYRDDDOYFKFPHLAVGF 417
DB 361 FOVLISIGLSLAIVALTSLGTLTLLNLTKRKAPHEAKYRDDDOYFKFPHLAVGF 417

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```

Oy      241  IYYAVAVSVWTAIIGSSSLAHPOGKISKTYGHSANVLPEGVAVDTSCHLIPSPWLPYVLGV 300
Db      241  IYYALAVSVWTAIIGSSSLAHPOGKISMTYHSANVLAVGVAVGTSCHLIPSPWLMVGLV 300
Oy      301  AGLISVRAKTLPGCCNPNVLGIPIHSSIMGNYPFSLGLLEETITTYLVLDYVGNNGMIG 360
Db      301  AGLISIGAKCGPGCCNPNVLGIPIDSSVMHYNFSLGLLEETITTYLVVYRHVWNGNGMIG 360
Oy      361  FOVLISGELSIAIVIALTSGLTALLLNKIKRAPHEAKKFPDQVFWKPFHLAVGF 417
Db      361  FOVLISMGELSLAIALTSGLTGLLNLIKWXAPHVAKYSDQVFWKPFHLAVGF 417

RESULT 8
137075
Rhesus-like protein - gorilla
C:Species: Gorilla gorilla (gorilla)
C:Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 09-Jul-2004
C:Accession: 137075
R:SalviGNOL, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie,
Biochem. Genet. 32, 201-221, 1994
A:Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the
A:Reference number: 137003; MUID:95085595; PMID:7993375
A:Accession: 137075
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-417 <RES>
C:Superfamily: human erythrocyte membrane protein Rhd
A:Cross-References: UNIPROT:Q28426; GB:LJ7052; NID:g607009; PIDN:AAA65626.1; PID:g607010

```

RESULT 9
184434
Rhesus-like protein - crab-eating macaque
C.Species: Macaca fascicularis (crab-eating macaque)
C.Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #next_change 09-Jul-2004
C.Accession: 184434
R.Salvignol, I.; Blancher, A.; Galvas, P.; Clayton, J.; Socha, W.W.; Colin, Y.; Ruffie,
Biochem. Genet. 32, 201-221, 1994
A.Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the
A.Reference number: 137003; PMID:95085595; PMID:7993375

A.Accession: I84434
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residues: 1-417 <RES>
A.Cross-references: UNIPROT:Q28481; GB:J37054; NID:ig609515; PIDN:AAA65628.1; PID:ig609516
C.Superfamily: human erythrocyte membrane protein Rhd

Query Match	71.0%	Score 1509;	DB 2;	Length 417;
Best Local Similarity	74.3%	Pred. No. 6e-113;		
Best Match 310; Conservative	31;	Mismatches	76;	Indels 0; Gaps 0;

```
QY      1  MSCKYPRSVORCLPLCATLTLEAAILLFFFTHYDASLEDOKGIVASYQVQODLTWMAI 600
      |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  MSCKYPRSVORCLPLMALTLLEAAILLFFFTTYDASLEDOKGIVASYQVQODLTWMAVL 600
```

```
QY      61 GLGFLTSSFRHSMSSVAFNLEMLALGVQWAILLDGFISQFPGSKVITLFSIMLATMSA 12
        ||||| : : : ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61 GLGFPFSLNRKRNSSSVAFNLEPLLALGVQWAILLDGFISQFSPGKVIKLFSIRLATRST 12
```

QY 121 LSVLSVDAVLGKVNLAQLVVMVLVEVTDLGNLRMVISNIFENTDHYMMNMHIYVFAAYFG 18

Db 121 TSMLSMNAVLGKVNLAQLVNMELVELTVFGTMRIVINIFKIDYGMNMHIHVFAPAYFG 18

```
QY      181 LTVAMCLPKPLBEGTEENDQRATIPSLAMGALFLMMRPVSVALLRSPIERKNAVFN 24
        |||||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 LTVAMCLPKPLPKGTEDKYOTTTSPSLPALMLGLTFLMMPWPTFNSALLNPIERKNAVS 24
```

QY 241 TYAAVAVSVTMAISGSLAHPOCKISKTYGHSAVLPEGAVDTSCHLIPSPWLPVIGLV 30
 ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 241 TYAALVASATMAISVSLSLAHPORKINMYMPNGLAGGAVGASCIVIHSPWIAMVGLV 30

OY 301 AGLSIVGAKYLPGCCNRVLGIPIHSSIMGYNFSLLGLLEEIIYYVLLVDITVGAGNMIG 36
| | | | | | | | | | : | : |
DB 301 AGLSISGAKCLPVCFNRVLGIHESHSMHYTFGLPALDEITYIYMALRYEAMSSMIG 36
| | | | | | | | | | : | : |

QY 361 FQVLISIGELSLAIVIALTSGILLTALLINKIRAPHEAKYFDQVFWKPPHLAVGF 417
| | | | : : : | | | | | | | | : | | | |
DH 361 FQVLISTGTSLIAMASTTSGLITGILINKIWGGPHVAKYFDDQAFWEPHILAVGF 417

RESULT 10
S78A80

Rhesus blood group antigen-like protein isoform 4 - human
C/Species: Homo sapiens (man)
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Jun-2001
C/Accession: G78480. 82550

R;Colin, Y.
submitted to the EMBL Data Library, November 1991
A;Reference number: S78478

A: Molecule type: mRNA
A: Residues: 1-354 <COL>
A: Cross-references: EMBL:X63098; NID:g36019; PIDN:CAA44812.1; PID:g36020

Blood 80, 1074-1078, 1992
A/Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing
A/Reference number: S26560; MUID:92360855; PMID:1379850

A;Molecule type: mRNA
A;Residues: 160-354 <LEV>
A;Cross-references: EMBL:X63098

C/Superfamily: human erythrocyte membrane protein RhD
C/keywords: alternative splicing; erythrocyte; surface antigen; transmembrane

Best Local Similarity 90.1%; Pred. No. 3.3e-105;
Matches 282; Conservative 10; Mismatches 21; Indels 0; Gaps

Db 1 MSSKPSRVRCLPLCALTEALILFLFFTHIDASLEQGLVASVQVGGLTVAAL 60

```

QY      61  GLGFLTSPRRHSSWSVAFLFMLALGVOMAILLDGFLSQPPSGKVITLPSIMLATMSA 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  CIGFLTSLNRRHSSWSVAFLFMLALGVOMAILLDGFLSQPPSGKVITLPSIRLATMSA 120
QY      121  LSVLISVDVAVLGNVLAQLVVMVLVEVTDLGNLRVVISNI FNTDYHMMNMHIYVFAAYFG 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  MSVLISAGAVLGNVLAQLVVMVLVEVTLGLTRVVISNI FNTDYHMMNRHYVFAAYFG 180
QY      181  LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
QY      241  TYVAAVSVVTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSGHLIPSPMLPIVLGLV 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241  TYVAAVSVVTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSGHLIPSPMLPIVLGLV 300
QY      301  AGLISVRGAKYLP 313
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301  AGLISIGAKCLP 313

```

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RESULT 11
137053
Rhesus-like protein - piliated gibbon
C/Species: Hylobates pileatus (piliated gibbon)
C/Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 09-Jul-2004
C/Accession: 137053
R/Salvignol, I.; Blancher, A.; Calvas, P.; Clayton, J.; Socha, W.W.; Collin, Y.; Ruffie,
Biochem. Genet. 32, 201-221, 1994
A/Title: Molecular genetics of chimpanzee Rh-related genes: their relationship with the
A/Reference number: 137003; MUID:9508595; PMID:7993375
A/Accession: 137053
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-354 <RES>
A/Cross-references: UNIPROT:Q28446; GB:U37051; NID:9607007; PIDN:AAA65625.1; PID:9607008
C/Superfamily: human erythrocyte membrane protein Rhd

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```

Query Match      60.9%; Score 1294; DB 2; Length 354;
Best Local Similarity 82.7%; Pred. No. 7,4e-96;
Matches 259; Conservative 20; Mismatches 34; Indels 0; Gaps 0;

QY      1  MSCKPSRVORCLPLCALTLTEAALILFFFTTHYDASLEDQGLVASVYOGDITVMAAI 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  MSSKTPSVRCCLPLMALTEAALILFFFTTHYDASLEDQGLVATYQVGDITVMAAL 60
QY      61  GLGFLTSPRRHSSWSVAFLFMLALGVOMAILLDGFLSQPPSGKVITLPSIMLATMSA 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GLGFLTSLNRRHSSWSVAFLFMLALGVOMAILLDGFLSQPPSGKVITLPSIRLATMSA 120
QY      121  LSVLISVDVAVLGNVLAQLVVMVLVEVTDLGNLRVVISNI FNTDYHMMNMHIYVFAAYFG 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  MSVLISAGAVLGNVLAQLVVMVLVEVTLGLTRVVISNI FNTDYHMMNRHYVFAAYFG 180
QY      181  LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  LTVAMCLPKPEPSTEDKEQIANSPSISAMLGALFLMIFPSPNSALLRSPIERKNAVEN 240
QY      241  TYVAAVSVVTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSGHLIPSPMLPIVLGLV 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241  TYVALAVSTVTAISVSLAHPQGIKSTYGHSAVLPEGVAVDTSGHLIPSPMLPIVLGLV 300
QY      301  AGLISVRGAKYLP 313
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301  AGLISIGAKCLP 313

```

```

RESULT 12
578479
Rhesus blood group antigen-like protein isoform VIII - human
C/Species: Homo sapiens (man)
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Jun-2001
C/Accession: 578479; S26563

```

```

R/Collin, Y.
submitted to the EMBL Data Library, November 1991
A/Reference number: 578478
A/Accession: 578479
A/Molecule type: mRNA
A/Residues: 1-266 <COL>
A/Cross-references: EMBL:X63096; NID:936044; PIDN:CAA44810.1; PID:936045
R/Le Van Kim, C.; Cherif-Zahar, B.; Raynal, V.; Mouro, I.; Lopez, M.; Carttron, J.P.; Coll
Blood 80, 1074-1078, 1992
A/Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing.
A/Reference number: S26560; MUID:92360855; PMID:1379850
A/Accession: S26563
A/Molecule type: mRNA
A/Residues: 160-266 <LEV>
A/Cross-references: EMBL:X63096
A/Experimental source: tissue-type bone marrow
C/Superfamily: human erythrocyte membrane protein Rhd
C/Keywords: alternative splicing; erythrocyte; surface antigen; transmembrane protein

```

```

Query Match      51.3%; Score 1089.5; DB 2; Length 266;
Best Local Similarity 58.0%; Pred. No. 1.2e-79;
Matches 242; Conservative 3; Mismatches 21; Indels 151; Gaps 1;

QY      1  MSCKPSRVORCLPLCALTLTEAALILFFFTTHYDASLEDQGLVASVYOGDITVMAAI 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1  MSSKTPSVRCCLPLCALTEAALILFFFTTHYDASLEDQGLVASVYOGDITVMAAI 60
QY      61  GLGFLTSPRRHSSWSVAFLFMLALGVOMAILLDGFLSQPPSGKVITLPSIMLATMSA 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61  GLGFLTSLNRRHSSWSVAFLFMLALGVOMAILLDGFLSQPPSGKVITLPSIRLATMSA 120
QY      121  LSVLISVDVAVLGNVLAQLVVMVLVEVTDLGNLRVVISNI FNTDYHMMNMHIYVFAAYFG 180
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121  MSVLISAGAVLGNVLAQLVVMVLVEVTLGLTRVVISNI FNTDYHMMNRHYVFAAYFG 180
QY      181  LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181  LTVAMCLPKPLPEGTEDNDQRAITPSLSAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
QY      241  TYVAAVSVVTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSGHLIPSPMLPIVLGLV 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241  TYVAAVSVVTAISGSSLAHPQGIKSTYGHSAVLPEGVAVDTSGHLIPSPMLPIVLGLV 300
QY      301  AGLISVRGAKYLP 313
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      301  AGLISIGAKCLP 313
QY      164  -----CONRVLGHHISVMSHSIFSLGILGELITVILVLAHTVMNGNMTG 209
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      164  -----CONRVLGHHISVMSHSIFSLGILGELITVILVLAHTVMNGNMTG 209
QY      210  FGVLISIGELIAIVIALTSGLTGLTLNLKIRKAPHEAKYFDQVFWKPHLAAGV 266
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      210  FGVLISIGELIAIVIALTSGLTGLTLNLKIRKAPHEAKYFDQVFWKPHLAAGV 266

```

```

RESULT 13
578478
Rhesus blood group antigen-like protein isoform VI - human
C/Species: Homo sapiens (man)
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 15-Jun-2001
C/Accession: 578478; S26562
R/Collin, Y.
submitted to the EMBL Data Library, November 1991
A/Reference number: 578478
A/Accession: 578478
A/Molecule type: mRNA
A/Residues: 1-267 <COL>
A/Cross-references: EMBL:X63095; NID:936042; PIDN:CAA44809.1; PID:936043
R/Le Van Kim, C.; Cherif-Zahar, B.; Raynal, V.; Mouro, I.; Lopez, M.; Carttron, J.P.; Coll
Blood 80, 1074-1078, 1992
A/Title: Multiple Rh messenger RNA isoforms are produced by alternative splicing.
A/Reference number: S26560; MUID:92360855; PMID:1379850
A/Accession: S26562
A/Molecule type: mRNA
A/Residues: 160-267 <LEV>
A/Cross-references: EMBL:X63095

```

A: Experimental source: tissue-type bone marrow
C: Superfamily: human erythrocyte membrane protein Rhd
E: Keywords: alternative splicing; erythrocyte; surface antigen; transmembrane protein

Query Match 47.1%; Score 1000.5; DB 2; Length 267;
Best Local Similarity 61.5%; Pred. No. 1.5e-72;
Matches 220; Conservative 7; Mismatches 26; Indels 105; Gaps 1;

```
QY 1 MSCKYPPSVORCLPLCLLTLEBALILFFFTTHDASLEDOKGLVASYQVGGDITVMAAI 60
DB 1 MSCKYPPSVORCLPLCLLTLEBALILFFFTTHDASLEDOKGLVASYQVGGDITVMAAI 60
QY 61 GLGFLTSFRRHSSVAFLFMLALGVQVAILLDGFLSQPPSGKVITLPSIMLATMSA 120
DB 61 GLGFLTSFRRHSSVAFLFMLALGVQVAILLDGFLSQPPSGKVITLPSIMLATMSA 120
QY 121 LSVLISVDAYLGVKNLAQLVVMVLVEYTDLGNLMVINSINIFNTDYHNMNMHIYVFAA 180
DB 121 MSVLISGAVLGVKNLAQLVVMVLVEYTDLGNLMVINSINIFNTDYHNMNMHIYVFAA 180
QY 181 LTVAMCLPKLPKESTENDQORATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 240
DB 181 LTVAMCLPKLPKESTENDQORATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 240
QY 163 ----- 162
DB 163 ----- 162
QY 241 TYVAVAVSVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
DB 241 TYVAVAVSVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
QY 163 ----- 195
DB 163 ----- 195
QY 301 AGHISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLVLDTVGANGNM 358
DB 196 AGHISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLVLDTVGANGNM 358
QY 196 AGHISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLVLDTVGANGNM 358
DB 196 AGHISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLVLDTVGANGNM 358
```

RESULT 14

S29124
membrane glycoprotein, 50K, erythrocyte - human
C: Species: Homo sapiens (man)
C: Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C: Accession: S29124; J0168
R: Ridgwell, K.; Spurt, N.K.; Laguda, B.; Macgeoch, C.; Arent, N.D.; Tanner, M.J.A.
Biochem. J. 287, 223-228, 1992
A: Title: Isolation of cDNA clones for a 50 kDa glycoprotein of the human erythrocyte mem
A: Reference number: S29124; MUID:93038558; PMID:1417776
A: Accession: S29124
A: Status: preliminary
A: Molecule type: mRNA
A: Residues: 1-409 <RID>
A: Cross-references: UNIPROT:Q02094; EMBL:X64594; NID:G31194; PIDN:CAA45883.1; PID:G31195
Biochem. Biophys. Res. Commun. 243, 233-240, 1998
A: Title: Identification of 5' flanking sequence of RH50 gene and the core region for ery
A: Reference number: J0168; MUID:98139897; PMID:9473510
A: Accession: J0168
A: Molecule type: mRNA
A: Residues: 1-52 <IMA>
C: Comment: This protein is membrane protein tightly associated with Rh polypeptides and
C: Gene: RH50
A: Superfamily: human erythrocyte membrane protein Rhd
C: Keywords: glycoprotein; transmembrane protein

Query Match 25.8%; Score 547.5; DB 2; Length 409;
Best Local Similarity 33.9%; Pred. No. 3.8e-36;
Matches 139; Conservative 79; Mismatches 111; Indels 21; Gaps 7;
QY 14 PLCLTLEBALILFFFTTHY--DASLEDOKGLVASYQV-----ODLTVMAIGL 62
DB 6 PLMAIVLEIMIVLFGFVEYETDQVTLBQNLNKKPDMGIFPELYLPQDVNMFVGF 65
QY 63 GLTTSFRRHSSVAFLFMLALGVQVAILLDGFLSQPPSGKVITLPSIMLATMSA 122
DB 66 GLTTSFRRHSSVAFLFMLALGVQVAILLDGFLSQPPSGKVITLPSIMLATMSA 124

```
QY 123 VLSVDAYLGVKNLAQLVVMVLVEYTDLGNLMVINSINIFNTDYHNMNMHIYVFAA 182
DB 125 VLSVDAYLGVKNLAQLVVMVLVEYTDLGNLMVINSINIFNTDYHNMNMHIYVFAA 184
QY 183 VAMCLPKLPKESTENDQORATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 242
DB 185 VAMCLPKLPKESTENDQORATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 244
QY 243 YAVAASVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 302
DB 245 YAVAASVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 304
QY 303 LISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLVLDTVGANGNM 361
DB 305 LISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLVLDTVGANGNM 360
QY 362 QVLSIGELSLAIVALTSGLLTALLNLKIRKAPHAAXYFDDQVFWKRP 411
DB 361 QVLSIGELSLAIVALTSGLLTALLNLKIRKAPHAAXYFDDQVFWKRP 406
```

RESULT 15

T29442
hypothetical protein F08F3.3 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C: Accession: T29442
R: Blanchard, M.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A: Description: The sequence of C. elegans cosmid F08F3.
A: Reference number: Z20620
A: Accession: T29442
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-463 <BLA>
A: Cross-references: UNIPROT:Q22947; EMBL:U64847; PIDN:AB04874.1; GSPDB:GN00023; CESP:F08
A: Experimental source: strain Bristol N2; clone F08F3
C: Gene: CESP:F08F3.3
A: Map position: 5
A: Intons: 18/3; 167/3; 266/3; 362/2; 442/3
C: Superfamily: human erythrocyte membrane protein Rhd

Query Match 19.4%; Score 412; DB 2; Length 463;
Best Local Similarity 26.6%; Pred. No. 2.9e-25;
Matches 116; Conservative 88; Mismatches 190; Indels 42; Gaps 8;

```
QY 10 QRCPLCALTEBALILFFFTTHYDAS-----LEDOKGLVASYQVGGDITVMAAI 61
DB 7 QRCPLCALTEBALILFFFTTHYDAS-----LEDOKGLVASYQVGGDITVMAAI 66
QY 62 LGLTTSFRRHSSVAFLFMLALGVQVAILLDGFLSQPPSGKVITLPSIMLATMSA 121
DB 67 LGLTTSFRRHSSVAFLFMLALGVQVAILLDGFLSQPPSGKVITLPSIMLATMSA 126
QY 122 SVLSVDAYLGVKNLAQLVVMVLVEYTDLGNLMVINSINIFNTDYHNM---NMHIYFAA 177
DB 127 SVLSVDAYLGVKNLAQLVVMVLVEYTDLGNLMVINSINIFNTDYHNM---NMHIYFAA 182
QY 178 YFGLTVAWCLPKLPKESTENDQORATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 237
DB 183 YFGLTVAWCLPKLPKESTENDQORATIPSLAMLGALFLMFRPSVNSALLRSPIERKKA 241
QY 238 VENTYVAASVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVL 297
DB 242 VENTYVAASVTATAGSSLAHPQGIKSTYGHSAVLPEGVAVDTSCHLIPSPMLPIVL 301
QY 298 GLVAGLISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLV----- 349
DB 302 GLVAGLISVGAAYLPGCCNRVLGIPHSIMGVNFSLLGLLEBIYIVLV----- 350
QY 350 --DTV--GANG-----MIGFOVLSIGELSLAIVALTSGLLTALLNLKIRKA 395
```

Db	362	OYDKIYPGWMARGEDRTRMFDEKTOALNOIMAIGLVFLASTV---	SGYLTGILLKUKINDQ	418
Oy	396	PHEAKYFDDQVFWKPP		411
		: : ::		
Db	419	VRDDEYADGDYFETP		434

Search completed: March 24, 2005, 13:17:05
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: March 24, 2005, 13:13:48 ; Search time 68 Seconds
(without alignments)
3140.250 Million cell updates/sec

Title: CAC07879
Predict score: 2124
Sequence: 1 MSCKYRSVRCPLCALTL.....EAKYFDQVFWKPHLAVGF 417

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1986	93.5	417	2	O6KC49
2	1981	93.3	417	2	O81ZT1
3	1980	93.2	417	2	Q7RU08
4	1978	93.1	417	2	O6SV89
5	1977	93.1	417	2	O6A1H2
6	1975	93.0	416	1	RHD_HUMAN
7	1975	93.0	417	2	O9UK19
8	1974	92.9	417	2	O6A1H3
9	1972	92.8	417	2	O6A1H4
10	1972	92.8	417	2	O9NXX8
11	1971	92.8	417	2	O6SV88
12	1970	92.7	417	2	O81ZT0
13	1970	92.7	417	2	O6SV90
14	1969	92.7	417	2	O6SV87
15	1969	92.7	417	2	O6SV91
16	1967	92.6	417	2	Q70HW2
17	1964.5	92.5	416	2	O6A1H1
18	1961	92.3	417	2	O99906
19	1957	92.1	417	2	O9CA07
20	1951	91.9	417	2	O9HCC3
21	1942	91.4	417	2	O9H248
22	1932	91.0	417	2	Q9UD25
23	1897	89.3	417	2	Q9UK74
24	1896	89.3	417	2	Q7Z594
25	1866	87.9	417	2	O81ZT5
26	1862	87.7	417	2	O9UPN0
27	1859	87.5	417	2	O6AZX5
28	1858	87.5	416	1	RHLR_PANTR
29	1855	87.3	417	2	O81ZT3
30	1855	87.3	417	2	O6J2U3
31	1849	87.1	417	2	Q7RU06

32	1845	86.9	417	2	O81ZT4	O81ZC4	homo sapien
33	1838	86.5	417	2	O81ZT2	O81ZC2	homo sapien
34	1837	86.5	416	1	RHLD_GORGO	Q284D7	gorilla gor
35	1835	86.4	416	1	RHLA_PANTR	Q28813	pan troglod
36	1828	86.1	416	1	RHCE_HUMAN	P18577	homo sapien
37	1806	85.0	416	1	RHLF_PANTR	Q28812	pan troglod
38	1798	84.7	416	1	RHLC_GORGO	Q28426	gorilla gor
39	1605	75.6	401	2	O6ZSC4	O6Z6C4	homo sapien
40	1526	71.8	407	2	O97525	O97525	pongo pygma
41	1519	71.5	416	1	RHL_MACMU	Q28813	macaca mulla
42	1504	70.8	416	1	RHL_MACFA	Q28481	macaca fasc
43	1493	70.3	398	2	O9UP91	O9UP91	homo sapien
44	1448	68.2	407	2	O97958	O97958	papio hamad
45	1412	66.5	405	2	O9TTF4	O9TTF4	cebus apell

ALIGNMENTS

RESULT 1	ID	PRELIMINARY	PRT	417 AA.
O6KC49	O6KC49			
AC	O6KC49			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DE	Rhesus blood group D antigen (Fragment).			
GN	Name=RHD;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Peripheral blood;			
RX	MEDLINE=93320449; PubMed=8329718;			
RA	Arce M.A., Thompson E.S., Wagner S., Coyne K.E., Ferdman B.A.,			
RA	Lublin D.M.;			
RT	"Molecular cloning of Rhd cDNA derived from a gene present in Rhd-			
RT	positive, but not Rhd-negative individuals.";			
RL	Blood 82:651-655 (1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Peripheral blood;			
RA	Doeschner A., Petershofen E.K., Schunter F., Wagner F.;			
RT	"New RHD alleles with previously unknown polymorphism.";			
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AJ704215; CAG28848.2; -			
DR	GO; GO:0016020; C:membrane; IEA.			
DR	InterPro; IPR002229; RhesusRHD.			
DR	InterPro; IPR010256; RH_like_transp.			
DR	Pfam; PF00909; Ammonium_transp. 1.			
FT	PRINTS; PR00342; RHESUSRHD.			
FT	NON_TER 417			
SQ	SEQUENCE 417 AA; 45124 MW; CBB643297E036559 CRC64;			
Query Match	93.5%; Score 1986; DB 2; Length 417;			
Best Local Similarity	95.2%; Pred. No. 3.9e-135;			
Matches	397; Conservative 4; Mismatches 16; Indels 0; Gaps 0;			
OY	1 MSCKYRSVRCPLCALTLLEALILFFFTHYDASLEDOKGLVASVYGQDITVAAI 60			
DB	1 MSCKYRSVRCPLCAVTLLEALILFFFTHYDASLEDOKGLVASVYGQDITVAAI 60			
OY	61 GLGFLTSSFRHSSVAFNLFMIALGVQVAIILDGFLSQPSGKVVITLFSIWLATWSA 120			
DB	61 GLGFLTSSFRHSSVAFNLFMIALGVQVAIILDGFLSQPSGKVVITLFSIWLATWSA 120			
OY	61 GLGFLTSSFRHSSVAFNLFMIALGVQVAIILDGFLSQPSGKVVITLFSIWLATWSA 120			
DB	61 GLGFLTSSFRHSSVAFNLFMIALGVQVAIILDGFLSQPSGKVVITLFSIWLATWSA 120			
OY	121 LSVLISVDVALGVNLAQLVVMVLVEVTDLGNRMVTSNIFNDDYHNMNMHIYFAAYFG 180			
DB	121 LSVLISVDVALGVNLAQLVVMVLVEVTDLGNRMVTSNIFNDDYHNMNMHIYFAAYFG 180			
OY	181 LTVAMCLPKPLPGTEDDNDORATIPSLASMLGALFLMMPSPVNSALLRSPIERKAVFN 240			

```
Db 181 LSVAMCPLPKPPEGTEDKDQATIPSLSAMLGALFLMFWPSPNSALLSPERKNAVN 240
QY 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLDEGVAVDTSCHLIPSPMLPIYGLV 300
Db 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLDEGVAVDTSCHLIPSPMLAMVLGLV 300
QY 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEETIYIVLVLDTVGANGMTG 360
Db 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEETIYIVLVLDTVGANGMTG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNKRKAPHEAKYFDDQYFWKPHLAVGF 417
Db 361 FOVLISIGELSLAIVIALTSGLLTALLNKRKAPHEAKYFDDQYFWKPHLAVGF 417
```

RESULT 2

```
081ZT1 PRELIMINARY; PRT; 417 AA.
ID 081ZT1
AC 081ZT1
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Rheus blood group D antigen D(667) variant.
OS Homo sapiens (Human).
OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22320945; PubMed=1293640; DOI=10.1182/blood-2002-01-0229;
RA Noizat-Pirenne F., Lee K., Le Pennec P.Y., Simon P., Kazup P.,
RA Roubert P., Koch R., Cartron J.P., Ancelet-Pirenne H.,
RT "Rare RHCE phenotypes in black individuals of Afro-Caribbean origin:
RT identification and transfusion safety."
RL Blood 100:4223-4231(2002)
RL EMBL; AF510069; AAN75125.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Ryanovirin-N.
DR InterPro; IPR002229; RhesusRHD.
DR Pfam; PF00909; Ammonium transp. 1.
DR PRINTS; PR00342; RHESUSRHD.
SQ SEQUENCE 417 AA; 45114 MW; C85D3A1ED5DA87 CRC64;
```

Query Match 93.3%; Score 1981; DB 2; Length 417;
Best Local Similarity 95.2%; Pred. No. 9e-135;
Matches 397; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

```
QY 1 MSCKYPRSVQRCPLCALTEBAALILFFFTHYDASLEDQKGLVASVQVGDITVMAAI 60
Db 1 MSCKYPRSVQRCPLCALTEBAALILFFFTHYDASLEDQKGLVASVQVGDITVMAAI 60
QY 61 GLGFLTSSFRHSSWSVAFLNFMALGVQWAILLDGFLSQPSPSKVITLFSIWLATMSA 120
Db 61 GLGFLTSSFRHSSWSVAFLNFMALGVQWAILLDGFLSQPSPSKVITLFSIWLATMSA 120
QY 121 LSVLISVDVAIVGKVNLAQLVVMVLEVTDLGNLMMVTSNIENFDYHNMNMHIYVFAAYFG 180
Db 121 LSVLISVDVAIVGKVNLAQLVVMVLEVTDLGNLMMVTSNIENFDYHNMNMHIYVFAAYFG 180
QY 181 LTVAMCPLPKPPEGTEDKDQATIPSLSAMLGALFLMFWPSPNSALLSPERKNAVN 240
Db 181 LTVAMCPLPKPPEGTEDKDQATIPSLSAMLGALFLMFWPSPNSALLSPERKNAVN 240
QY 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLDEGVAVDTSCHLIPSPMLPIYGLV 300
Db 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLDEGVAVDTSCHLIPSPMLAMVLGLV 300
QY 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEETIYIVLVLDTVGANGMTG 360
Db 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEETIYIVLVLDTVGANGMTG 360
```

```
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNKRKAPHEAKYFDDQYFWKPHLAVGF 417
Db 361 FOVLISIGELSLAIVIALTSGLLTALLNKRKAPHEAKYFDDQYFWKPHLAVGF 417
```

RESULT 3

```
QY 07RU08 PRELIMINARY; PRT; 417 AA.
ID 07RU08
AC 07RU08
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Rhd protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21898876; PubMed=11902138; DOI=10.1182/blood-2001-12-0153;
RA Wagner F.F., Flegel W.A.;
RT "RHCE represents the ancestral RH position, while RHD is the
RT duplicated gene."
RL Blood 99:2272-2273(2002).
CC -1- MISCCELLANEOUS: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ third party annotation (TPA) entry.
DR EMBL; BN000065; CAD29848.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Ryanovirin-N.
DR InterPro; IPR002229; RhesusRHD.
DR Pfam; PF00909; Ammonium transp. 1.
DR PRINTS; PR00342; RHESUSRHD.
SQ SEQUENCE 417 AA; 45180 MW; 649F1BFA664AE7DB CRC64;
```

Query Match 93.2%; Score 1980; DB 2; Length 417;
Best Local Similarity 95.2%; Pred. No. 1.1e-134;
Matches 397; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

```
QY 1 MSCKYPRSVQRCPLCALTEBAALILFFFTHYDASLEDQKGLVASVQVGDITVMAAI 60
Db 1 MSCKYPRSVQRCPLCALTEBAALILFFFTHYDASLEDQKGLVASVQVGDITVMAAI 60
QY 61 GLGFLTSSFRHSSWSVAFLNFMALGVQWAILLDGFLSQPSPSKVITLFSIWLATMSA 120
Db 61 GLGFLTSSFRHSSWSVAFLNFMALGVQWAILLDGFLSQPSPSKVITLFSIWLATMSA 120
QY 121 LSVLISVDVAIVGKVNLAQLVVMVLEVTDLGNLMMVTSNIENFDYHNMNMHIYVFAAYFG 180
Db 121 LSVLISVDVAIVGKVNLAQLVVMVLEVTDLGNLMMVTSNIENFDYHNMNMHIYVFAAYFG 180
QY 181 LTVAMCPLPKPPEGTEDKDQATIPSLSAMLGALFLMFWPSPNSALLSPERKNAVN 240
Db 181 LTVAMCPLPKPPEGTEDKDQATIPSLSAMLGALFLMFWPSPNSALLSPERKNAVN 240
QY 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLDEGVAVDTSCHLIPSPMLPIYGLV 300
Db 241 TYAAVAASVVTATISGSSLAHPQCKISTYGHSAVLDEGVAVDTSCHLIPSPMLAMVLGLV 300
QY 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEETIYIVLVLDTVGANGMTG 360
Db 301 AGLISVGAKYLPGCCNRVLGIPHSSIMGNFSLGLLEETIYIVLVLDTVGANGMTG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNKRKAPHEAKYFDDQYFWKPHLAVGF 417
Db 361 FOVLISIGELSLAIVIALTSGLLTALLNKRKAPHEAKYFDDQYFWKPHLAVGF 417
```

RESULT 4
06SV89 PRELIMINARY; PRT; 417 AA.

Query Match	Best Local Similarity	93.1%;	Score 1977;	DB 2;	Length 417;
Matches 396;	Conservative 4;	Mismatches 17;	Indels 0;	Gaps 0;	
RT	"Four new RHD alleles with previously unknown polymorphism."				
RL	Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AJ784331; CAH04921.1; "				
DR	GO; GO:0016020; C:membrane; IEA.				
DR	InterPro; IPR011058; Cytochrome-N.				
DR	InterPro; IPR002229; RhesusRHD.				
DR	InterPro; IPR010256; RH_like_transp.				
DR	Pfam; PF00909; Ammonium_transp; 1.				
DR	PRINTS; PR00342; RHESUSRHD.				
FT	NON TER	1	1		
FT	NON TER	417	417		
SO	SEQUENCE	417 AA;	45212 MW;	649F1BF6364AF7D0	CRC64;
Query Match	93.1%;	Score 1977;	DB 2;	Length 417;	
Best Local Similarity	95.0%;	Pred. No. 1.8e-114;			
Matches 396;	Conservative 4;	Mismatches 17;	Indels 0;	Gaps 0;	
QY	1	MSCKYPSVQRCPLCALTELEAAILLFPFPTHDALEDOQGLVASYQVGQDILTWAAI	60		
DB	1	MSSKYPSPVRCLPLMALTEAAILLFPFPTHDALEDOQGLVASYQVGQDILTWAAI	60		
QY	61	GLGFITSSFRHSNSSVAFNLFMLALGVQMAILLDFISOPPSGKVVITLPSIMATMSA	120		
DB	61	GLGFITSSFRHSNSSVAFNLFMLALGVQMAILLDFISOPPSGKVVITLPSILATMSA	120		
QY	121	LSVLISDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVPAAYFG	180		
DB	121	LSVLISDAVLGKYNLAQLVVMVLEVTDLGNLRMVISNIFNTDYHNMNMHIYVPAAYFG	180		
QY	181	LTVAMCPLKPLPEGETENDQDAITPSISANLGLFLMMFRSVNSALIRSTIERKAVEN	240		
DB	181	LSVMACPLKPLPEGETEDDQDAITPSISANLGLFLMMFRSVNSALIRSTIERKAVEN	240		
QY	241	TYVAVAASVVAIAIGSSSLAHQOKISKTYGHSAYLPEGVAVDTSCHLIPSPMLPIVGLV	300		
DB	241	TYVAVAASVVAIAIGSSSLAHQOKISKTYGHSAYLPEGVAVDTSCHLIPSPMLPIVGLV	300		
QY	301	AGLISVGAAXKLPSCCNKRVLGIPHSSIMGVNFSLGLLEELIYVLLVLDTVGANGNIG	360		
DB	301	AGLISVGAAXKLPSCCNKRVLGIPHSSIMGVNFSLGLLEELIYVLLVLDTVGANGNIG	360		
QY	361	FOVLLSTIGELSLAIVIALTSGLLTALLINKIRKAPHEAKYFDQVFWKPHLAVGF	417		
DB	361	FOVLLSTIGELSLAIVIALTSGLLTALLINKIRKAPHEAKYFDQVFWKPHLAVGF	417		
RESULT 6					
RHD_HUMAN	STANDARD;	PRT;	416 AA.		
AC	Q02161; Q02162; Q07618; Q16147; Q16235; Q16355; Q9NPK0; Q9UQ20;				
AC	Q9UQ21; Q9UQ22; Q9UQ23;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	05-JUN-2004 (Rel. 44, Last annotation update)				
DE	Blood group Rh(D) polypeptide (Rhesus D antigen) (RHXIII) (Rh				
DE	polypeptide 2) (Rhpr1).				
GN	Name=RHD;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_Taxid=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				
RX	MEDLINE=93066356; PubMed=1438298;				
RA	le van Kim C., Mouro I., Cherif-Zahar B., Raynal V., Cherrier C.,				
RA	Catron U.-P., Colin Y.;				
RT	"Molecular cloning and primary structure of the human blood group Rhd				
RT	polypeptide";				
RL	Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929 (1992).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Bone marrow;				

RX MEDLINE=92360855; PubMed=1379850;
 RA le van Kim C., Cherif-Zahar B., Raynal V., Mouro I., Lopez M.,
 RA Cartton J.-P., Colin Y.;
 RT "Multiple Rh messenger RNA isoforms are produced by alternative
 RT splicing.";
 RL Blood 80:1074-1078 (1992).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93320449; PubMed=8329718;
 RA Arce M.A., Thompson E.S., Wagner S., Coyne K.E., Ferdman B.A.,
 RA Lublin D.M.;
 RT "Molecular cloning of RHD cDNA derived from a gene present in RHD-
 RT positive, but not Rhd-negative individuals.";
 RL Blood 82:651-655 (1993).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93316282; PubMed=7916743;
 RA Kajii E., Umenishi F., Iwamoto S., Ikemoto S.;
 RT "Isolation of a new cDNA clone encoding an Rh polypeptide associated
 RT with the Rh blood group system.";
 RL Hum. Genet. 91:157-162 (1993).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=953329738; PubMed=7606008;
 RA Huang C.-H., Reid M.E., Chen Y.;
 RT "Identification of a partial internal deletion in the RH locus causing
 RT the human erythrocyte D-phenotype.";
 RL Blood 86:784-790 (1995).
 [6]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=94235883; PubMed=8180407;
 RA Westhoff C.M., Wylie D.E.;
 RT "Identification of a new RHD-specific mRNA from K562 cells.";
 RL Blood 83:3098-3100 (1994).
 [7]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RX MEDLINE=94362249; PubMed=8080999;
 RA Suyama K., Lunn R., Haller S., Goldstein J.;
 RT "Rh(D) antigen expression and isolation of a new Rh(D) cDNA isoform in
 RT human erythroleukemic K562 cells.";
 RL Blood 84:1975-1981 (1994).
 [8]
 RP SEQUENCE FROM N.A., AND VARIANTS VAL-222; GLN-232; MET-237 AND
 RP LEU-244.
 RA Hyodo H., Ishikawa Y., Kashiwase K., Ogawa A., Watanabe Y.,
 RA Tsuneyama H., Toyoda C., Uchikawa M., Akaza T., Fujii T.;
 RT "Polymorphisms of Rhdva to the EMBL/GenBank/DBJ databases."
 RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 [9]
 RP VARIANT BLOOD GROUP TAR.
 RX MEDLINE=95259709; PubMed=7741145;
 RA Rouillac C., le van Kim C., Beolet M., Cartton J.-P., Colin Y.;
 RT "leu110Pro substitution in the Rhd polypeptide is responsible for the
 RT Dv11 category blood group phenotype.";
 RL Am. J. Hematol. 49:87-88 (1995).
 -1- FUNCTION: May be part of an oligomeric complex which is likely to
 have a transport or channel function in the erythrocyte membrane.
 -1- SUBCELLULAR LOCATION: Integral membrane protein.
 -1- ALTERNATIVE PRODUCTS:
 Event=Alternative splicing; Named isoforms=3;
 Name=1; Synonyms=Long;
 IsoId=002161-1; Sequence=Displayed;
 Name=2; Synonyms=Short 1;
 IsoId=002161-2; Sequence=VSP_005706;
 Name=3; Synonyms=Short 2;
 IsoId=002161-3; Sequence=VSP_005707, VSP_005708;
 -1- TISSUE SPECIFICITY: Restricted to tissues or cell lines expressing
 erythroid characters.
 -1- POLYMORPHISM: RHD and RHCE are responsible for the Rh blood group
 system. The molecular basis of the Tar-Rh40 blood group antigen is
 a polymorphism in position 109.
 -1- SIMILARITY: Belongs to the Rh family.

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CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
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CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X63097; CAA44811.1; -
DR	EMBL; X63094; CAA44808.1; -
DR	EMBL; L08429; AAA02679.1; -
DR	EMBL; S57971; AAB36081.1; -
DR	EMBL; S78509; AAB34852.1; -
DR	EMBL; S70174; AAB30756.1; -
DR	EMBL; S73913; AAB31911.1; -
DR	EMBL; AB018966; BAA81899.1; -
DR	EMBL; AB018967; BAA81900.1; -
DR	EMBL; AB018968; BAA81901.1; -
DR	EMBL; AB018969; BAA82159.1; -
DR	PIR; A46368; A46368.
DR	PIR; I52615; I52615.
DR	Genew; HGNC:10093; RHD.
DR	MIM; 116880;
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.
DR	InterPro; IPRO101058; CyanoVillin-N.
DR	InterPro; IPRO10256; RH like transpc.
DR	Pfam; PF00909; Ammonium transp; 1.
DR	PRINTS; PR00342; RHESUSRD.
KM	Alternative splicing; Blood group antigen; Erythrocyte; Polymorphism;
KM	Transmembrane.
FT	INIT_MEN 0
FT	TRANSMEM 11 31 Potential.
FT	TRANSMEM 43 63 Potential.
FT	TRANSMEM 76 96 Potential.
FT	TRANSMEM 106 126 Potential.
FT	TRANSMEM 129 149 Potential.
FT	TRANSMEM 166 186 Potential.
FT	TRANSMEM 202 222 Potential.
FT	TRANSMEM 237 257 Potential.
FT	TRANSMEM 286 306 Potential.
FT	TRANSMEM 333 353 Potential.
FT	TRANSMEM 357 377 Potential.
FT	VARSPLIC 313 408 Missing (in isoform 2).
FT	VARSPLIC 315 315 /FtId=VSP_005706.
FT	VARSPLIC 316 416 C-> S (in isoform 3).
FT	VARIANT 109 109 /FtId=VSP_005707.
FT	VARIANT 109 109 Missing (in isoform 3).
FT	VARIANT 217 217 /FtId=VSP_005708.
FT	VARIANT 217 217 L-> P (in Tar antigen).
FT	VARIANT 217 217 /FtId_VAR_006919.
FT	VARIANT 217 217 M-> I.
FT	VARIANT 222 222 /FtId=VAR_006920.
FT	VARIANT 222 222 F-> V (in RhDva (FK) and RhDva (TT)).
FT	VARIANT 232 232 /FtId=VAR_013304.
FT	VARIANT 232 232 E-> Q (in RhDva (FK), RhDva (TO),
FT	VARIANT 237 237 RhDva (TT) and RhDvo).
FT	VARIANT 237 237 /FtId=VAR_013305.
FT	VARIANT 237 237 V-> M (in RhDva (TO) and RhDva (TT)).
FT	VARIANT 237 237 /FtId=VAR_013306.
FT	VARIANT 244 244 V-> L (in RhDva (TT)).
FT	VARIANT 244 244 /FtId=VAR_013307.
FT	VARIANT 15 15 W-> C (in Ref. 5).
FT	VARIANT 38 38 E-> G (in Ref. 4).
FT	VARIANT 102 102 S-> P (in Ref. 4).
FT	VARIANT 126 126 V-> A (in Ref. 4).
FT	VARIANT 173 173 V-> M (in Ref. 5).
FT	VARIANT 181 181 S-> T (in Ref. 4).
FT	VARIANT 313 313 G-> V (in Ref. 4 and 7).
FT	VARIANT 322 322 P-> H (in Ref. 4).
FT	VARIANT 397 397 E-> V (in Ref. 5).
FT	VARIANT 416 AA: 45049 MW: 91360 pI: 3.75 Mr: 97500
FT	SEQUENCE 416 AA: 45049 MW: 91360 pI: 3.75 Mr: 97500

Query Match 93.0%; Score 1975; DB 1; Length 416;
Best Local Similarity 95.2%; Pred. No. 2.4e-134;
Matches 396; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2 SCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAIG 61
DB 1 SSKYPSVRRCPLMALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAIG 60
QY 62 LGFLTSSFRHSHSSVAFMLALGVQMAILLDGLSQFPGSKVITLFSRLATMSA 121
DB 61 LGFLTSSFRHSHSSVAFMLALGVQMAILLDGLSQFPGSKVITLFSRLATMSA 120
QY 122 SVLISVDVALGKVNLAQVVMVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 181
DB 121 SVLISVDVALGKVNLAQVVMVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180
QY 182 TVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 241
DB 181 SVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
QY 242 YYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIVLGLVA 301
DB 241 YYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIVLGLVA 300
QY 302 GLISVVGAKYLPGCCNRVLGIPHSSIMGYNPSLLGLEEIIYIVLVLDVTGAGNGMIG 361
DB 301 GLISVVGAKYLPGCCNRVLGIPHSSIMGYNPSLLGLEEIIYIVLVLDVTGAGNGMIG 360

RESULT 7
Q9UK19 PRELIMINARY; PRT; 417 AA.
ID Q9UK19
AC Q9UK19
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2004 (TReMBLrel. 26, Last annotation update)
DE Rhd type Iiia protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97398395; Pubmed=9256293;
RA Huang C.H., Chen Y., Reid M.;
RT "Human D(IIia) erythrocytes: Rhd protein is associated with multiple
RT dispersed amino acid variations.";
RL Am. J. Hematol. 55:139-145(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Huang C.H.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF187846; AF04565.1; -.
DR PIR; I54193; I54193.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; CyanoVitrin-N.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR010256; RH_like_transp.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHEUSRHD.
SQ SEQUENCE 417 AA; 45273 MW; 491FB1FE1BA37957 CRC64;

Query Match 93.0%; Score 1975; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 2.4e-134;
Matches 396; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAI 60
DB 1 MSCKYPSVORCLPLMALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAAL 60

QY 61 GLGFLTSSFRHSHSSVAFMLALGVQMAILLDGLSQFPGSKVITLFSRLATMSA 120
DB 61 GLGFLTSSFRHSHSSVAFMLALGVQMAILLDGLSQFPGSKVITLFSRLATMSA 120
QY 121 LSVLISVDVALGKVNLAQVVMVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180
DB 121 LSVLISVDVALGKVNLAQVVMVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
DB 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240
QY 241 TTYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
DB 241 TTYAAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
QY 301 AGLISVVGAKYLPGCCNRVLGIPHSSIMGYNPSLLGLEEIIYIVLVLDVTGAGNGMIG 360
DB 301 AGLISVVGAKYLPGCCNRVLGIPHSSIMGYNPSLLGLEEIIYIVLVLDVTGAGNGMIG 360
QY 361 FOVLISIGELSLAIVALTSGLLTGLLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVALTSGLLTGLLNLKIRKAPHEAKYFPDQVFWKPHLAVGF 417

RESULT 8
Q6A1H3 PRELIMINARY; PRT; 417 AA.
ID Q6A1H3
AC Q6A1H3
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Rhesus Blood group D antigen (Fragment).
GN Name=RHD;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Doescher A., Wagner F., Schunter F., Petershofen B.K.;
RT "Four new RHD alleles with previously unknown polymorphism.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ784310; CAH04920.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; CyanoVitrin-N.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR010256; RH_like_transp.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHEUSRHD.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 417 AA; 45146 MW; 649F1358664AF7DB CRC64;

Query Match 92.9%; Score 1974; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 2.9e-134;
Matches 396; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAI 60
DB 1 MSCKYPSVORCLPLMALTEALILFFFTHYDASLEDOKGLVASYQVGODLTWMAI 60
QY 61 GLGFLTSSFRHSHSSVAFMLALGVQMAILLDGLSQFPGSKVITLFSRLATMSA 120
DB 61 GLGFLTSSFRHSHSSVAFMLALGVQMAILLDGLSQFPGSKVITLFSRLATMSA 120
QY 121 LSVLISVDVALGKVNLAQVVMVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180
DB 121 LSVLISVDVALGKVNLAQVVMVLVEVTDLGNLRVINSINFTDYHNMNMHIYFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNAVEN 240

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Db      181 LSVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPEGVA|VDTSCHL|IPSPML|PIY|GLV 300
      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPGVA|VGTSCHL|IPSPML|AV|GLV 300
Qy      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
Db      361 FOVLISIGELSLA|VIALV|ALTSGL|LTALL|NLK|IRK|APHEAKY|PDDQV|FWK|P|HL|AVGF 417
      361 FOVLISIGELSLA|VIALV|ALTSGL|LTALL|NLK|IRK|APHEAKY|PDDQV|FWK|P|HL|AVGF 417

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RESULT 9

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O6A1H4 ID Q6A1H4 PRELIMINARY; PRT; 417 AA.
AC      25-OCT-2004 (TREMBlrel. 28, Created)
DT      25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT      25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE      Rhesus blood group D antigen (Fragment).
GN      Name=RHD;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Peripheral blood;
RA      Doescher A., Wagner F., Schunter F., Petershofen E.K.;
RL      Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ784309; CAH04919.1; -
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR011058; CyanoVirlin-N.
DR      InterPro; IPR022229; RhesuSRHD.
DR      InterPro; IPR010256; RH like transp.
DR      Pfam; PF00909; Ammonium transp; 1.
DR      PRINTS; PR00342; RHEUSRHD.
FT      NON_TER 1
FT      NON_TER 1
SQ      SEQUENCE 417 AA; 45171 MW; 449F15CA664AF365 CRC64;

```

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Query Match      92.8%; Score 1972; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 4e-134;
Matches 396; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

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Qy      1 MSCKYPRSVQRCLP|CAITL|EAL|ILFLFYPTHYDAS|LEDQK|GLV|AS|YQV|GODL|TVMA|I 60
      1 MSCKYPRSVQRCLP|MALTL|EAL|ILFLFYPTHYDAS|LEDQK|GLV|AS|YQV|GODL|TVMA|I 60
Db      61 GLGFLTSSFRHSSWSVA|FNL|FML|ALGVQMA|ILDG|FLSQ|PSPGKV|ITL|FS|IRL|ATMSA 120
      61 GLGFLTSSFRHSSWSVA|FNL|FML|ALGVQMA|ILDG|FLSQ|PSPGKV|ITL|FS|IRL|ATMSA 120
Qy      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
Db      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
Qy      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
Db      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
Qy      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPEGVA|VDTSCHL|IPSPML|PIY|GLV 300
      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPGVA|VGTSCHL|IPSPML|AV|GLV 300
Db      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPGVA|VGTSCHL|IPSPML|AV|GLV 300
      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPGVA|VGTSCHL|IPSPML|AV|GLV 300
Qy      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
Db      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360

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Qy      361 FOVLISIGELSLA|VIALV|ALTSGL|LTALL|NLK|IRK|APHEAKY|PDDQV|FWK|P|HL|AVGF 417
      361 FOVLISIGELSLA|VIALV|ALTSGL|LTALL|NLK|IRK|APHEAKY|PDDQV|FWK|P|HL|AVGF 417
Db

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RESULT 10

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O9NXV8 ID Q9NXV8 PRELIMINARY; PRT; 417 AA.
AC      01-OCT-2000 (TREMBlrel. 15, Created)
DT      01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT      01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE      Rhesus blood group D antigen.
GN      Name=RHD;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Wagner F.F., Flegel W.A.;
RL      Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AJ287289; CAB75731.1; -
DR      EMBL; AJ287290; CAB75731.1; JOINED.
DR      EMBL; AJ287291; CAB75731.1; JOINED.
DR      EMBL; AJ287292; CAB75731.1; JOINED.
DR      EMBL; AJ287293; CAB75731.1; JOINED.
DR      EMBL; AJ287294; CAB75731.1; JOINED.
DR      EMBL; AJ287295; CAB75731.1; JOINED.
DR      EMBL; AJ287296; CAB75731.1; JOINED.
DR      EMBL; AJ287297; CAB75731.1; JOINED.
DR      EMBL; AJ287298; CAB75731.1; JOINED.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR011058; CyanoVirlin-N.
DR      InterPro; IPR022229; RhesuSRHD.
DR      InterPro; IPR010256; RH like transp.
DR      Pfam; PF00909; Ammonium transp; 1.
DR      PRINTS; PR00342; RHEUSRHD.
SQ      SEQUENCE 417 AA; 45210 MW; 60FB4CPB16F163EF CRC64;

```

```

Query Match      92.8%; Score 1972; DB 2; Length 417;
Best Local Similarity 95.0%; Pred. No. 4e-134;
Matches 396; Conservative 3; Mismatches 18; Indels 0; Gaps 0;

```

```

Qy      1 MSCKYPRSVQRCLP|CAITL|EAL|ILFLFYPTHYDAS|LEDQK|GLV|AS|YQV|GODL|TVMA|I 60
      1 MSCKYPRSVQRCLP|MALTL|EAL|ILFLFYPTHYDAS|LEDQK|GLV|AS|YQV|GODL|TVMA|I 60
Db      61 GLGFLTSSFRHSSWSVA|FNL|FML|ALGVQMA|ILDG|FLSQ|PSPGKV|ITL|FS|IRL|ATMSA 120
      61 GLGFLTSSFRHSSWSVA|FNL|FML|ALGVQMA|ILDG|FLSQ|PSPGKV|ITL|FS|IRL|ATMSA 120
Qy      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
Db      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
      121 LSVLISVDAV|GKVN|LAQ|LVVMV|VEVTD|GNL|RMV|IS|NI|FNTD|YHNM|MH|IY|FAA|YFG 180
Qy      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
Db      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
      181 LTVAMC|PKPLPEGTEDKQGTATIPSLSAM|GLFLFMFWP|SNSALLSP|ERKNA|VN 240
Qy      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPEGVA|VDTSCHL|IPSPML|PIY|GLV 300
      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPGVA|VGTSCHL|IPSPML|AV|GLV 300
Db      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPGVA|VGTSCHL|IPSPML|AV|GLV 300
      241 TTYAAVAVSVTTAISGSSLAHPQCKISKTYGHS|AVLPGVA|VGTSCHL|IPSPML|AV|GLV 300
Qy      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
Db      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360
      301 AGLISVGA|KYLPGCCNR|VLGI|PHSS|IMGYN|FSL|GL|EBE|I|Y|VL|V|DTV|GA|NGM|G 360

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RESULT 11
06SV88      PRELIMINARY;      PRT;      417 AA.
AC 06SV88;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Rhesus blood group D antigen DRO (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirenne F., Ansaert-Pirenne H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449384; AAR24081.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR01058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRD.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHESUSRD.
DR NON TER
SQ SEQUENCE 417 AA; 45148 MW; CBSA4464DBDAF6BD CRC64;

Query Match      92.8%; Score 1971; DB 2; Length 417;
Best Local Similarity 94.7%; Pred. No. 4,7e-134;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASVYQGDITVMAAI 60
DB 1 MSCKYPSVORCLPLMALTEALILFFFTHYDASLEDOKGLVASVYQGDITVMAAI 60
QY 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSILATMSA 120
DB 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSILATMSA 120
QY 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
DB 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
QY 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
DB 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
QY 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
DB 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
QY 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
DB 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
QY 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
QY 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
QY 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
QY 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNKIRKAPHEAKYFPDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLLTALLNKIRKAPHEAKYFPDQVFWKPHLAVGF 417

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RP SEQUENCE FROM N.A.
RX MEDLINE=2320945; PubMed=12393640; DOI=10.1182/blood-2002-01-0229;
RA Noizat-Pirenne F., Lee K., Le Penne P.Y., Simon P., Kaup P.,
RA Bachir D., Rouzeau A.M., Roussel M., Juszcak G., Menneteau C.,
RA Rouger P., Kotb R., Cartton J.P., Ansaert-Pirenne H.;
RT "Rare RHEC phenotypes in black individuals of Afro-Caribbean origin:
RT identification and transfusion safety."
RL Blood 100:4223-4231 (2002).
DR EMBL; AF510070; AAN75126.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR01058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRD.
DR InterPro; IPR010256; RH_like_transp.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHESUSRD.
SQ SEQUENCE 417 AA; 45222 MW; 85241934D7F382D0 CRC64;

Query Match      92.7%; Score 1970; DB 2; Length 417;
Best Local Similarity 94.7%; Pred. No. 5.6e-134;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILFFFTHYDASLEDOKGLVASVYQGDITVMAAI 60
DB 1 MSCKYPSVORCLPLMALTEALILFFFTHYDASLEDOKGLVASVYQGDITVMAAI 60
QY 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSILATMSA 120
DB 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILLDGFLSQPSGKVITLFSILATMSA 120
QY 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
DB 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
QY 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
DB 121 LSVLISVDALGVKNLAQLVVMVLEVTDLGNLRMVISNIFNTDYNHNMHIYFAAYFG 180
QY 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
DB 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
QY 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
DB 181 LTVAMCLPKLPBCTEDNDQATIPSLSAMLGALFLMFPSPVNSALLRPIERKAVFN 240
QY 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
QY 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
DB 241 TYAAVAVSVTTAISGSSLAHPQCKISKTYGHSVLPBGVAVDTSCHLIPSPMLPIYGLV 300
QY 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
QY 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
DB 301 AGLISVGAKYLPCCNCRVLGIPHSSIMGYNFSILGLLEIYIVLVLDVTGANGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLLTALLNKIRKAPHEAKYFPDQVFWKPHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLLTALLNKIRKAPHEAKYFPDQVFWKPHLAVGF 417

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RESULT 12
081ZT0      PRELIMINARY;      PRT;      417 AA.
AC 081ZT0;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Rhesus blood group D antigen D (674) variant.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RESULT 13
06SV90      PRELIMINARY;      PRT;      417 AA.
AC 06SV90;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Rhesus blood group D antigen DLO (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirenne F., Ansaert-Pirenne H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449382; AAR24079.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR01058; Cytochrome-N.
DR InterPro; IPR002229; RhesusRD.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHESUSRD.

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FT  NON TER      417      417
SQ  SEQUENCE      417 AA; 45188 MW; 0B49654D7994CIDE CRC64;

Query Match
Best Local Similarity 92.7%; Score 1970; DB 2; Length 417;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY  1 MSCKYPRSVORCLPFCALTELEAAILLFFFTHYDASLEDOKGLVASYOVGODLTVMMAI 60
DB  1 MSCKYPRSVORCLPFCALTELEAAILLFFFTHYDASLEDOKGLVASYOVGODLTVMMAI 60
QY  61 GIGFLTSSFRHSWSSVAFNLFMLALGVQMAILLDGFLSQFPSGKVITLFSIWLATMSA 120
DB  61 GIGFLTSSFRHSWSSVAFNLFMLALGVQMAILLDGFLSQFPSGKVITLFSIWLATMSA 120
QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
DB  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
DB  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
QY  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
DB  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
DB  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417
DB  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417

RESULT 14
Q6SV87 PRELIMINARY; PRT; 417 AA.
AC Q6SV87;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Rhesus blood group D antigen DBA (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirene F.; Ansart-Pirene H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449385; AAR24082.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Cyanovirin-N.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR010256; RH_like_transpt.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHSDUSRHD.
FT NON TER      417
SQ SEQUENCE      417 AA; 45146 MW; C37E02699A8BBE90 CRC64;

Query Match
Best Local Similarity 92.7%; Score 1969; DB 2; Length 417;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY  1 MSCKYPRSVORCLPFCALTELEAAILLFFFTHYDASLEDOKGLVASYOVGODLTVMMAI 60
DB  1 MSCKYPRSVORCLPFCALTELEAAILLFFFTHYDASLEDOKGLVASYOVGODLTVMMAI 60
QY  61 GIGFLTSSFRHSWSSVAFNLFMLALGVQMAILLDGFLSQFPSGKVITLFSIWLATMSA 120
DB  61 GIGFLTSSFRHSWSSVAFNLFMLALGVQMAILLDGFLSQFPSGKVITLFSIWLATMSA 120
QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
DB  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
DB  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
QY  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
DB  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
DB  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417
DB  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417
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QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
DB  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
DB  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
QY  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
DB  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
DB  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417
DB  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417

RESULT 15
Q6SV91 PRELIMINARY; PRT; 417 AA.
AC Q6SV91;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Rhesus blood group D antigen DBA (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Noizat-Pirene F.; Ansart-Pirene H.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY449381; AAR24078.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR011058; Cyanovirin-N.
DR InterPro; IPR002229; RhesusRHD.
DR InterPro; IPR010256; RH_like_transpt.
DR Pfam; PF00909; Ammonium_transp; 1.
DR PRINTS; PR00342; RHSDUSRHD.
FT NON TER      417
SQ SEQUENCE      417 AA; 45220 MW; C84B08C4780D3DCC CRC64;

Query Match
Best Local Similarity 92.7%; Score 1969; DB 2; Length 417;
Matches 395; Conservative 4; Mismatches 18; Indels 0; Gaps 0;

QY  1 MSCKYPRSVORCLPFCALTELEAAILLFFFTHYDASLEDOKGLVASYOVGODLTVMMAI 60
DB  1 MSCKYPRSVORCLPFCALTELEAAILLFFFTHYDASLEDOKGLVASYOVGODLTVMMAI 60
QY  61 GIGFLTSSFRHSWSSVAFNLFMLALGVQMAILLDGFLSQFPSGKVITLFSIWLATMSA 120
DB  61 GIGFLTSSFRHSWSSVAFNLFMLALGVQMAILLDGFLSQFPSGKVITLFSIWLATMSA 120
QY  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
DB  121 LSVLISVDVAVLGVKNIQAQLVVMVLVEVTDLGNLRMVINSINFTDYHMMMH1YVFAAYFG 180
QY  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
DB  181 LTVAMCLPKPLPEGTEDNDQATIPSLSNMGLALFLMFRPSVNSALRSPIERKNAVEN 240
QY  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
DB  241 TYAAVAVSVVTA1SGSSLAHPQKISKTYHSAVLPEGVAVDTSCHLIPSPWLPIYGLV 300
QY  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
DB  301 AGLISVRGAKYLPGCCNRVLGIPHSSIMGVNSFLGLLEIITYVLLVLDTVGAGNGMTG 360
QY  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417
DB  361 FOVLISIGELSLAIVIALTSGLLTALLMLKIRKAPHEAKYPDDQVFMKPHLAVGF 417
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Db	301	AGLISVGAKYLPCCNRVLGIPIHSSIMGYNFSLSGLGELIYIVLVLDIVGAGNGMIG	360
QY	361	FQVLLSIGELSLAIVIALTSGLLTALLLNKIRKAPHEAKYFDDQVFWKPPHLAVGF	417
Db	361	FQVLLSIGELSLAIVIALTSGLLTALLLNKIRKAPHEAKYFDDQVFWKPPHLAVGF	417

Search completed: March 24, 2005, 13:18:18
Job time : 70 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 24, 2005, 13:13:45 ; Search time 164 Seconds
(without alignments)
983.409 Million cell updates/sec

Title: CAC07879
Perfect score: 2124
Sequence: 1 MSCKPRSYGRCLPLCALTL.....EAKYFDQYFWKPHLVAGF 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1982	93.3	417	3	AAB03341
2	1980	93.2	417	2	AAV24056
3	1975	93.0	416	7	ADBS4449
4	1975	93.0	416	7	ADDA5097
5	1975	93.0	416	7	ADBS4445
6	1932	91.0	417	7	ADDA6525
7	1932	91.0	417	7	ADDA6529
8	1859	87.5	417	3	AA803339
9	1854	87.3	417	3	AA803338
10	1838	86.5	417	3	AA803342
11	1833	86.3	417	3	AA803340
12	1605	75.6	401	8	ADRO9337
13	991.5	46.7	422	7	ADDA6523
14	991.5	46.7	422	7	ADBS4447
15	991.5	46.7	422	7	ADBS4443
16	991.5	46.7	422	7	ADDA5095
17	991.5	46.7	422	7	ADDA6527
18	913.5	43.0	209	8	ADP29742
19	882	41.5	214	8	ADP29767
20	497	23.4	473	3	AA842135
21	497	23.4	479	4	AA829656
22	497	23.4	479	4	AA837000
23	497	23.4	479	5	AAU78997
24	497	23.4	479	6	ABU56530
25	497	23.4	479	8	ADN04910

26	490	23.1	445	6	AB015004	Ab015004 Human NOV
27	488.5	23.0	498	5	AAU78998	AAU78998 Mouse Rh
28	480.5	22.6	455	5	AAU78092	AAU78092 Mouse non
29	476	22.4	324	7	ADJ69283	AdJ69283 Human hea
30	466.5	22.0	458	5	AAU78091	AAU78091 Human non
31	418.5	19.7	441	5	ABP69263	ABP69263 Human pol
32	417	19.6	449	5	ABBS7883	Abbs7883 Drosophila
33	374	17.6	448	5	AAE18217	AAE18217 Human MOL
34	374	17.6	448	7	ADJ18212	AdJ18212 Human mol
35	362.5	17.1	395	7	ADSO8355	AdSO8355 Novel pro
36	302	14.2	326	5	ABBS9036	Abbs9036 Human pol
37	257	12.1	54	4	AAAM15110	AAm15110 Peptide #
38	257	12.1	54	4	ABBS4104	Abbs4104 Peptide #
39	257	12.1	54	4	AAW27565	AAW27565 Peptide #
40	257	12.1	54	4	ABR28933	ABr28933 Peptide #
41	257	12.1	54	4	ABBI9542	ABb19542 Protein #
42	257	12.1	54	4	AAW67271	AAW67271 Human bon
43	257	12.1	54	4	AAW54889	AAW54889 Human bra
44	257	12.1	54	4	ABG48932	ABg48932 Human liv
45	257	12.1	54	4	AAW02851	AAW02851 Peptide #

ALIGNMENTS

RESULT 1					
AA803341	AA803341 standard; protein; 417 AA.				
ID	AA803341				
XX	AA803341;				
AC	26-SEP-2000 (first entry)				
DT	Human Rhd protein.				
XX	Human; rhesus blood group system; Rh; Rhd; RHCE; sickle cell disease; thalassemia; Rhc; Rho; RHe; RHe; alloimmunisation prevention; human immune Rh haemolytic disease; rhesus protein; immunosuppressive; vaccine.				
XX	Homo sapiens.				
OS	WO200032632-A2.				
PN	08-JUN-2000.				
PD	01-DEC-1999; 99WO-GB004027.				
PF	01-DEC-1998; 98GB-00026378.				
XX	(UYAB-) UNIV ABERDEEN				
PA	(COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.				
XX	Urbanlak SJ, Barker RN;				
PI	WPI; 2000-412291/35.				
XX	Composition for prevention of alloimmunization or immunosuppression of a response elicited by alloimmunization or an autoimmune hemolytic disease, comprises an epitope of a rhesus protein.				
PT	Disclosure; Page 88-90; 92pp; English.				
PS	Human blood contains the rhesus (Rh) blood group system, and humans can either be RhD positive or negative. This can lead to complications during transfusions or pregnancy if RhD negative individuals are exposed to RhD positive blood, leading to them becoming immunised to produce anti-D. The present invention relates to new human allo- and auto-reactive T-cell epitopes (AAV99760-Y99769 and AAB03201-B03337) from RhD, RhC, RhE, and Rho proteins. These epitopes bind to T-cells to elicit an immune response, i.e. immunisation. These epitopes can be used as a vaccine for the prevention of alloimmunisation or immunosuppression of a response elicited by alloimmunisation or an autoimmune hemolytic disease.				

CC Examples of autoimmune haemolytic diseases are sickle cell disease and
CC thalassemia. The present sequence is the human Rhd protein from which
CC the epitopes in the present invention were derived
XX

SO Sequence 417 AA;

Query Match 93.3%; Score 1982; DB 3; Length 417;
Best Local Similarity 95.2%; Pred. No. 4.4e-184;
Matches 397; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 MSCKYRSVORCLPCLATLEAALLILFFFTHYDASLEDQGLVASYQVGODLTVMMAI 60
DB 1 MSCKYRSVORCLPCLATLEAALLILFFFTHYDASLEDQGLVASYQVGODLTVMMAI 60
QY 61 GLGFLTSSFRHSSWSSVAFNLFMALGVOMAILLDGFLSOPFSKGVVITLPSIMLATMSA 120
DB 61 GLGFLTSSFRHSSWSSVAFNLFMALGVOMAILLDGFLSOPFSKGVVITLPSIRLATMSA 120
QY 121 LSVLISVDVAVLGKVNLAQLVWVAVVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180
DB 121 LSVLISVDVAVLGKVNLAQLVWVAVVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNVFN 240
DB 181 LTVAMCLPKPLPEGTEDNDQRTATIPSLAMLGALFLMFRPSVNSALLRSPIERKNVFN 240
QY 241 TYAAVAVSVVTAISGSSLAHPQGISKTYGHSVAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
DB 241 TYAAVAVSVVTAISGSSLAHPQGISKTYGHSVAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
QY 301 AGLISVRAKYLPGCCNVVLGIPIHSSINGNPSLIGLLEIITVYLVLDTVGAGNGMIG 360
DB 301 AGLISVGAKTYPGCCNVVLGIPIHSSINGNPSLIGLLEIITVYLVLDTVGAGNGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417

RESULT 2

AAV24056
ID AAV24056 standard; protein; 417 AA.

AC AAV24056;

DT 04-OCT-1999 (first entry)

DE Protein encoded by the prevalent allele of the Rhd gene.

KW Allele; Rhesus D antigen; Rhd; weak D phenotype; blood transfusion.

OS Homo sapiens.

FN WO9937763-A2.

PD 29-JUL-1999.

PF 18-DEC-1998; 98WO-EP008319.

PR 23-JAN-1998; 98EP-00101203.

PA (DRKB-) DRK BLUTSPENDEDIENST BADEN WUERTTEMBERG.

PI Flegel WA, Wagner FF;

DR WPI; 1999-469127/39.

XX N-PSDB; AAX86522.

PT Nucleic acid sequences correlated with Rhesus weak D phenotype, useful
XX for screening blood from donors and recipients for transfusion methods.

PS Disclosure; Fig 2; 64pp; English.
XX

CC The present sequence is encoded by the prevalent allele of the Rhesus D
CC (Rhd) antigen gene. The specification describes a Rhd contributing to or
CC indicative of the weak D phenotype, where the Rhd polynucleotide carries
CC at least one missense mutation as compared to the wild-type Rhd, in its
CC transmembrane and/or intracellular regions, especially in amino acid
CC positions 2-16, 114-149, 179-225 or/and 267-397, with the proviso that
CC the D antigen does not carry a single missense mutation leading to a
CC F223V or T281S substitution. The probes and antibodies are useful in the
CC methods for detection of weak D phenotypes. Red blood cells, from
CC probands, are useful for the assessment of the affinity, avidity and/or
CC reactivity of monoclonal anti-D antibodies, polyclonal anti-D antisera
CC of anti-globulin or anti-human-globulin antisera. Detecting the presence
CC of the Rhd associated with weak D phenotype is useful for determining
CC that a patient in need of a blood transfusion is to be transfused with
CC Rhd negative blood from a donor. Alternatively, testing for weak D
CC phenotype Rhd in the blood of a donor is useful for determining whether
CC the donor blood should be excluded for transfusion to patients having
CC wild type Rhd or weak D types, other than that of the donor weak D type
XX

SO Sequence 417 AA;

Query Match 93.2%; Score 1980; DB 2; Length 417;
Best Local Similarity 95.2%; Pred. No. 6.8e-184;
Matches 397; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 1 MSCKYRSVORCLPCLATLEAALLILFFFTHYDASLEDQGLVASYQVGODLTVMMAI 60
DB 1 MSCKYRSVORCLPCLATLEAALLILFFFTHYDASLEDQGLVASYQVGODLTVMMAI 60
QY 61 GLGFLTSSFRHSSWSSVAFNLFMALGVOMAILLDGFLSOPFSKGVVITLPSIMLATMSA 120
DB 61 GLGFLTSSFRHSSWSSVAFNLFMALGVOMAILLDGFLSOPFSKGVVITLPSIRLATMSA 120
QY 121 LSVLISVDVAVLGKVNLAQLVWVAVVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180
DB 121 LSVLISVDVAVLGKVNLAQLVWVAVVETDLGNLRVVISNIFNTDYHMMMHIIYFAAYFG 180
QY 181 LTVAMCLPKPLPEGTEDNDORATIPSLAMLGALFLMFRPSVNSALLRSPIERKNVFN 240
DB 181 LTVAMCLPKPLPEGTEDNDQRTATIPSLAMLGALFLMFRPSVNSALLRSPIERKNVFN 240
QY 241 TYAAVAVSVVTAISGSSLAHPQGISKTYGHSVAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
DB 241 TYAAVAVSVVTAISGSSLAHPQGISKTYGHSVAVLPEGVAVDTSCHLIPSPMLPIVLGLV 300
QY 301 AGLISVRAKYLPGCCNVVLGIPIHSSINGNPSLIGLLEIITVYLVLDTVGAGNGMIG 360
DB 301 AGLISVGAKTYPGCCNVVLGIPIHSSINGNPSLIGLLEIITVYLVLDTVGAGNGMIG 360
QY 361 FOVLISIGELSLAIVIALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417
DB 361 FOVLISIGELSLAIVIALTSGLTGLNLNLKIRKAPHEAKYFDQVFWKPFHLAVGF 417

RESULT 3

ADE54449
ID ADE54449 standard; protein; 416 AA.

AC ADE54449;

DT 29-JAN-2004 (first entry)

DE Human Protein Q9UQ21, SEQ ID NO 252.

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;
XX spared nerve injury; SNI; Chung.

OS Homo sapiens.

PN WO2003016475-A2.

PD 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Coetigan M;
PI WPI; 2003-268312/26.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying a sequence
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

XX Sequence 416 AA;

Query Match 93.0%; Score 1975; DB 7; Length 416;

Best Local Similarity 95.2%; Pred. No. 2.1e-183;

Matches 396; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2 SCKYPRSVORCLPLCALTLBAALLLFYFTHYDASLEDOGVAASYQVGGDLTVMAAIG 61
DB 1 SSKYPRSVORCLPLMALTLBAALLLFYFTHYDASLEDOGVAASYQVGGDLTVMAAIG 60
QY 62 LGFTTSFRRHSSWVAFNLMALGVQWALLDGFISQPSGKVITLPSIRATMSAL 121
DB 61 LGFTTSFRRHSSWVAFNLMALGVQWALLDGFISQPSGKVITLPSIRATMSAL 120
QY 122 SVLISVAVALGVKVALQVLVWVLEVTDLGLRMVINSINFTDVMHMMHYYFAAFGL 181
DB 121 SVLISVAVALGVKVALQVLVWVLEVTDLGLRMVINSINFTDVMHMMHYYFAAFGL 180
QY 182 TVAMCLPEKPEEGEDNDORATIPSLSAMLGALFLMFRPSVNSALLRSPERKNAVENT 241
DB 181 SVAMCLPEKPEEGEDNDORATIPSLSAMLGALFLMFRPSVNSALLRSPERKNAVENT 240
QY 242 YYAAVAVSVYTAISGSSSLAHPOGKISKTYGSHAVPEGAADVTSCHLIPSPMLPVGLGVA 301
DB 241 YYAAVAVSVYTAISGSSSLAHPOGKISKTYGSHAVPEGAADVTSCHLIPSPMLPVGLGVA 300

QY 302 GLISVGRAXYLPCCNRVILGIPHSSIMGVNFSLGLLEBIIYVLLVLDTVGAGNGMIGF 361
DB 301 GLISVGRAXYLPCCNRVILGIPHSSIMGVNFSLGLLEBIIYVLLVLDTVGAGNGMIGF 360
QY 362 QVLSIGELSLAIVALTSGLTALLINKIRAPHEAKYFDQVFWKPHLAVGF 417
DB 361 QVLSIGELSLAIVALTSGLTALLINKIRAPHEAKYFDQVFWKPHLAVGF 416

RESULT 4

ADD45097
ID ADD45097 standard; protein; 416 AA.

AC ADD45097;

DT 29-JAN-2004 (first entry)

XX Human Protein Q9UQ21, SEQ ID NO 10529.

XX Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

PN W02003016475-A2.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GENO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

PI Woolf C, D'urso D, Befort K, Coetigan M;

XX WPI; 2003-268312/26.

XX Claim 1; Page; 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a

CC method for identifying a compound or small molecule that regulates the

CC activity in an animal of one or more of the polypeptides given in the

CC specification, a method for identifying a compound useful in treating

CC pain and a pharmaceutical composition comprising the one or more

CC polypeptides or their antibodies. The polynucleotide or the compound that

CC modulates its activity is useful for preparing a medicament for treating

CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction

CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene

CC therapy). The sequence presented is a human protein (shown in Table 2 of

CC the specification) which is differentially expressed during pain. Note:

CC The sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 416 AA;

Query Match 93.0%; Score 1975; DB 7; Length 416;
Best Local Similarity 95.2%; Pred. No. 2.1e-183;
Matches 396; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2 SCKYPRSVORCLPLCALTLLEAALLLFYFFTHYDASLEBQKLVASVYQGDULTWMAAG 61
DB 1 SSKYPRSVORCLPLMALTLLEAALLLFYFFTHYDASLEBQKLVASVYQGDULTWMAAG 60
QY 62 LGFLTSSFRHSHWSSVAEFLFMALGVQWAILLDGFLSQPSGKVITLFSIWLATMSAL 121
DB 61 LGFLTSSFRHSHWSSVAEFLFMALGVQWAILLDGFLSQPSGKVITLFSIWLATMSAL 120
QY 122 SVLISVDVAVLGKVNLAQLVVMVLVEVTDLGNLRMTISINFTDYMNMNMHTYVFAAYGGL 181
DB 121 SVLISVDVAVLGKVNLAQLVVMVLVEVTDLGNLRMTISINFTDYMNMNMHTYVFAAYGGL 180
QY 182 TVAMCLPKPLPEGTEDNDQRATIPSLISAMLGALFLMFRPVSNSALLRSPIERKNAVFNT 241
DB 181 SVAMCLPKPLPEGTEDNDQRATIPSLISAMLGALFLMFRPVSNSALLRSPIERKNAVFNT 240
QY 242 YVAVAVSVVTAISGSSLAHPQKISKTYGHSVAVLEBGAVADTSCHLISPMWLPYVLGLVA 301
DB 241 YVAVAVSVVTAISGSSLAHPQKISKTYGHSVAVLEBGAVADTSCHLISPMWLPYVLGLVA 300
QY 302 GLISVGAKEYLPGCCNRVLGIPHSIMGVNFSLLGLEIITYVLVLDVTGAGNGMIGF 361
DB 301 GLISVGAKEYLPGCCNRVLGIPHSIMGVNFSLLGLEIITYVLVLDVTGAGNGMIGF 360
QY 362 QVLLSIGELSLAIVALTSGLLTALLNLKIRKAPHEAKYFPDDQVFWKPHLAVGF 417
DB 361 QVLLSIGELSLAIVALTSGLLTALLNLKIRKAPHEAKYFPDDQVFWKPHLAVGF 416

RESULT 5
ADES4445
ID ADE54445 standard; protein; 416 AA.

XX ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

XX AC ADE54445;

PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX

SQ Sequence 416 AA;

Query Match 93.0%; Score 1975; DB 7; Length 416;
Best Local Similarity 95.2%; Pred. No. 2.1e-183;
Matches 396; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 2 SCKYPRSVORCLPLCALTLLEAALLLFYFFTHYDASLEBQKLVASVYQGDULTWMAAG 61
DB 1 SSKYPRSVORCLPLMALTLLEAALLLFYFFTHYDASLEBQKLVASVYQGDULTWMAAG 60
QY 62 LGFLTSSFRHSHWSSVAEFLFMALGVQWAILLDGFLSQPSGKVITLFSIWLATMSAL 121
DB 61 LGFLTSSFRHSHWSSVAEFLFMALGVQWAILLDGFLSQPSGKVITLFSIWLATMSAL 120
QY 122 SVLISVDVAVLGKVNLAQLVVMVLVEVTDLGNLRMTISINFTDYMNMNMHTYVFAAYGGL 181
DB 121 SVLISVDVAVLGKVNLAQLVVMVLVEVTDLGNLRMTISINFTDYMNMNMHTYVFAAYGGL 180
QY 182 TVAMCLPKPLPEGTEDNDQRATIPSLISAMLGALFLMFRPVSNSALLRSPIERKNAVFNT 241
DB 181 SVAMCLPKPLPEGTEDNDQRATIPSLISAMLGALFLMFRPVSNSALLRSPIERKNAVFNT 240
QY 242 YVAVAVSVVTAISGSSLAHPQKISKTYGHSVAVLEBGAVADTSCHLISPMWLPYVLGLVA 301
DB 241 YVAVAVSVVTAISGSSLAHPQKISKTYGHSVAVLEBGAVADTSCHLISPMWLPYVLGLVA 300
QY 302 GLISVGAKEYLPGCCNRVLGIPHSIMGVNFSLLGLEIITYVLVLDVTGAGNGMIGF 361
DB 301 GLISVGAKEYLPGCCNRVLGIPHSIMGVNFSLLGLEIITYVLVLDVTGAGNGMIGF 360
QY 362 QVLLSIGELSLAIVALTSGLLTALLNLKIRKAPHEAKYFPDDQVFWKPHLAVGF 417
DB 361 QVLLSIGELSLAIVALTSGLLTALLNLKIRKAPHEAKYFPDDQVFWKPHLAVGF 416

RESULT 6
ADD46525
ID ADD46525 standard; protein; 417 AA.

XX ADD46525;

XX ADD46525;

XX ADD46525;

XX ADD46525;

XX ADD46525;

XX Human Protein CAB09722, SEQ ID NO 12206.
DE
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS unidentified.
XX
PN WO2003016475-A2.
PD
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; CAB09722.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Example 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp://ipo.int/pub/published_pct_sequences.
XX
XX Sequence 417 AA;
SQ

Query Match 91.0%; Score 1932; DB 7; Length 417;
Best Local Similarity 92.6%; Pred. No. 3.2e-179;
Matches 386; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

1 MSCQVPSVGRCPGLCALTEALILFYPFTHYDASLEQKGVASVYGQDITWAAI 60
1 MSSKTPSSVRKCPMLTLERAILILFFTHRDASLEQKGVASVYGQDITWAAI 60
61 GLGFLTSSFRRHSSVAFNLFMLALGVQWAILLDGFLSQFPGKVITLFSIRLATMSA 120

Db 61 GLGFLTSSFRRHSSVAFNLFMLALGVQWAILLDGFLSQFPGKVITLFSIRLATMSA 120
Qy 121 LSTVLISVDVAGKVNLAQLVWMTLVEVTDLGNLRMTISNIFNTDYHNNMHIVFAAYFG 180
Db 121 MSTVLISAGAVLAGVNLALQVWMTLVEVTALGTLRMVYSNIFNTDYHNNLHFVFAAYFG 180
Qy 181 LTVAMCLPKRPLEPGETDNDORATIPSLASMLGALFLMFPSPVNSALLRSPIRKNAVFN 240
Db 181 LTVAMCLPKRPLEPGETDNDORATIPSLASMLGALFLMFPSPVNSALLRSPIRKNAVFN 240
Qy 241 TTYAAVSVVTTAISGSSLAHPQGIKITYGSHAVLEBGAVDTSCHLIPSPMLPIVLGLV 300
Db 241 TTYAAVSVVTTAISGSSLAHPQGIKISMTYVHSAVLGAVGTSCHLIPSPMLAMVLGLV 300
Qy 301 AGLISVRGAKYLPGCCNRVLGITHSSIMGNFSLGLBEITITVLLVDTVAGNGMTG 360
Db 301 AGLISIGGAKCLPGCCNRVLGIPHSSIMGNFSLGLGIIYIVLLVDTVAGNGMTG 360
Qy 361 FOYVLISIGELSLAIVALTSGLTALLNLKIRKAPHEAKYFPDQYFWKRPPLAVGF 417
Db 361 FOYVLISIGELSLAIVALTSGLTLLNLKIRKAPHEAKYFPDQYFWKRPPLAVGF 417

RESULT 7
ADD46529
ID ADD46529 standard; protein; 417 AA.
XX
AC ADD46529;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein CAB09722, SEQ ID NO 12210.
XX
XX Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
XX Homo sapiens.
OS unidentified.
XX
PN WO2003016475-A2.
PD
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
PA
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; CAB09722.
XX
PT New composition comprising two or more isolated polypeptides, useful for
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XX
PS Example 1; Page: 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal

[illegible]

Oy	301	GLISVRAKXLPQCNVNRVGIPISSISGVSFLLGLEELIYIYLVLDPYGAQNGMIG	360
	:	:	
Db	301	AGLISIGAKCLPVCCNKNVLGIHHISVMSHSTFSLGLGELTYIYLVLAHTVWNGMIG	360
	:	:	
Oy	361	FOVLISIGELSLAIYALITSGLLTALNLTKIRKAPHAKEYFPDQVFWKFPHLAVGF	417
	:	:	
Db	361	FOVLISIGELSLAIYALITSGLLTGLNLTKIKAPHAKEYFPDQVFWKFPHLAVGF	417
	:	:	
	RESULT 10		
	ID	AA033342	standard; protein: 417 AA.
AC	AA033342;		
XX			
DT	26-SEP-2000	(first entry)	
XX			
DE	Human Rhce protein.		
KW	Human; rhesus blood group system; Rh, Rhd, Rhce; sickle cell disease;		
KM	thalassaemia; Rhc; Rhd; Rhe; alloimmunisation prevention;		
KW	autoimmune Rh haemolytic disease; rhesus protein; immunosuppressive;		
XX	vaccine.		
XX			
OS	Homo sapiens.		
PN	WO200032632-A2.		
XX			
PD	08-JUN-2000.		
XX			
PF	01-DEC-1999;	99WO-GB004027.	
XX			
PR	01-DEC-1998;	98GB-00026378.	
XX			
PA	(UYAB-) UNIV ABERDEEN.		
BA	(COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.		
PI	Urbanjak SJ, Barker RN;		
XX			
DR	WPI; 2000-412291/35.		
PT	Composition for prevention of alloimmunization or immunosuppression of a		
PT	response elicited by alloimmunization or an autoimmune hemolytic disease,		
XX	comprises an epitope of a rhesus protein.		
PS	Disclosure; Page 90-92; 92pp; English.		
XX			
CC	Human blood containing the rhesus (Rh) blood group system, and humans can		
CC	either be Rhd positive or negative. This can lead to complications during		
CC	transfusions or pregnancy if Rhd negative individuals are exposed to Rhd		
CC	positive blood, leading to them becoming immunised to produce anti-D. The		
CC	present invention relates to new human allo- and auto-reactive T-cell		
CC	epitopes (AA199760-199769 and AA03201-03337) from RHD, Rhc, RHC, RHE		
CC	and RHE proteins. These epitopes bind to T-cells to elicit an immune		
CC	response, i.e. immunisation. These epitopes can be used as a vaccine for		
CC	the prevention of alloimmunisation or immunosuppression of a response		
CC	elicited by alloimmunisation or an autoimmune haemolytic disease.		
CC	Examples of autoimmune haemolytic diseases are sickle cell disease and		
CC	thalassaemia. The present sequence is the human Rhce protein from which		
XX	the epitopes in the present invention were derived		
XX			
SQ	Sequence 417 AA;		
	Query Match	86.5%; Score 1838; DB 3; Length 417;	
	Best Local Similarity	89.0%; Pred. No. 4.7e-170;	
	Matches 371; Conservative 12; Mismatches 34; Indels 0; Gaps 0		
Oy	1	MSCKYPRSVORCLPLCALTEEAAILLFYFTTHYDASLEDDKGLVASYQVGODLTVMMAI	60
	:	:	
Db	1	MSKXPRSVORCLPLMLTTEAAILLFYFTTHYDASLEDDKGLVASYQVGODLTVMMAI	60
	:	:	
Oy	61	GLGLTSSFRHSHSSVAFNIPMLALGYQVAILLDGFLSQSPSGKVVITLFSIMLATMSA	120
	:	:	

Db 61 GLGFLTSNFRHSMSSVAFNLFMLALGVMAILLDGFLSQPPGKVITLFSIRLATMSA 120
 QY 121 LSVLISVDALVGVNLAQVVMVLVEVTDLGNLRMTISINFTDYMNMNHIVFAAYFG 180
 Db 121 MSVLISAGAVLGKVNLAQVVMVLVEVTDLGNLRMTISINFTDYMNMNRHFVFAAYFG 180
 QY 181 LTVAMCLPKPLPGTEEDNDQRTIPSLSAMLGALFLMFRPVSNSALRSPIERKAAVFN 240
 Db 181 LTVAMCLPKPLPGTEEDNDQRTIPSLSAMLGALFLMFRPVSNSALRSPIERKAAVFN 240
 QY 241 TYAAVAVSVVTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300
 Db 241 TYAAVAVSVVTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300
 QY 301 AGLISVRGAKYLPGCCNRVLGIPIHSSIMGVNFSLGLEEIIYIYLVLDVTGAGNGMIG 360
 Db 301 AGLISGAKCLPVCNCRVLGIHHSVMHSIFSLGLGLEIYIYLVLDVTGAGNGMIG 360
 QY 361 FOVLISIGLSLAIVALTSGLLTALLNLKTRKAPHEAKYFDDQVFWKFPHLAVGF 417
 Db 361 FOVLISIGLSLAIVALTSGLLTALLNLKTRKAPHEAKYFDDQVFWKFPHLAVGF 417

RESULT 11

AAB03340

ID AAB03340 standard; protein; 417 AA.

AC AAB03340;

DT 26-SEP-2000 (first entry)

DE Human Rhce protein.

KM Human; rhesus blood group system; Rh; Rhd; Rhce; sickle cell disease;
 KW thalassemia; Rhc; Rhg; Rhe; alloimmunisation prevention;
 KW autoimmune Rh haemolytic disease; rhesus protein; immunosuppressive;
 vaccine.

OS Homo sapiens.

PN WO200032632-A2.

PD 08-JUN-2000.

PF 01-DEC-1999; 99WO-GB004027.

PR 01-DEC-1998; 98GB-00026378.

PA (UYAB-) UNIV ABERDEEN.

PA (COMM-) COMMON SERVICES AGENCY SCOTTISH HEALTH S.

PI Urbanlak SJ, Barker RN;

XX WPI; 2000-412291/35.

Composition for prevention of alloimmunization or immunosuppression of a
 response elicited by alloimmunization or an autoimmune hemolytic disease,
 comprises an epitope of a rhesus protein.

PS Disclosure; Page 86-88; 92pp; English.

Human blood contains the rhesus (Rh) blood group system, and humans can
 either be Rhd positive or negative. This can lead to complications during
 transfusions or pregnancy if Rhd negative individuals are exposed to Rhd
 positive blood, leading to them becoming immunised to produce anti-D. The
 present invention relates to new human allo- and auto-reactive T-cell
 epitopes (AAV99760-Y99769 and AAB03201-B03337) from Rhd, Rhc, Rhe, RHE
 and RHE proteins. These epitopes bind to T-cells to elicit an immune
 response, i.e. immunisation. These epitopes can be used as a vaccine for
 the prevention of alloimmunisation or immunosuppression of a response
 elicited by alloimmunisation or an autoimmune hemolytic disease.
 CC Examples of autoimmune hemolytic diseases are sickle cell disease and
 CC thalassemia. The present sequence is the human Rhce protein from which

CC the epitopes in the present invention were derived
 XX SQ Sequence 417 AA;

Query Match 86.3%; Score 1833; DB 3; Length 417;
 Best Local Similarity 98.7%; Pred. No. 1,4e-169;
 Matches 370; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 1 MSCKYPSVORCLPLCALTEALILLFYPTHYDASLEDQGVASVGVGDLYTMAAI 60
 Db 1 MSCKYPSVORCLPLCALTEALILLFYPTHYDASLEDQGVASVGVGDLYTMAAI 60
 QY 61 GLGFLTSNFRHSMSSVAFNLFMLALGVMAILLDGFLSQPPGKVITLFSIRLATMSA 120
 Db 61 GLGFLTSNFRHSMSSVAFNLFMLALGVMAILLDGFLSQPPGKVITLFSIRLATMSA 120
 QY 121 LSVLISVDALVGVNLAQVVMVLVEVTDLGNLRMTISINFTDYMNMNHIVFAAYFG 180
 Db 121 MSVLISAGAVLGKVNLAQVVMVLVEVTDLGNLRMTISINFTDYMNMNRHFVFAAYFG 180
 QY 181 LTVAMCLPKPLPGTEEDNDQRTIPSLSAMLGALFLMFRPVSNSALRSPIERKAAVFN 240
 Db 181 LTVAMCLPKPLPGTEEDNDQRTIPSLSAMLGALFLMFRPVSNSALRSPIERKAAVFN 240
 QY 241 TYAAVAVSVVTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300
 Db 241 TYAAVAVSVVTAISGSSLAHPQCKISKTGSHAVLPBGVAVDTSCHLIPSPMLPIVLGLV 300
 QY 301 AGLISVRGAKYLPGCCNRVLGIPIHSSIMGVNFSLGLEEIIYIYLVLDVTGAGNGMIG 360
 Db 301 AGLISGAKCLPVCNCRVLGIHHSVMHSIFSLGLGLEIYIYLVLDVTGAGNGMIG 360
 QY 361 FOVLISIGLSLAIVALTSGLLTALLNLKTRKAPHEAKYFDDQVFWKFPHLAVGF 417
 Db 361 FOVLISIGLSLAIVALTSGLLTALLNLKTRKAPHEAKYFDDQVFWKFPHLAVGF 417

RESULT 12

ADR09337

ID ADR09337 standard; protein; 401 AA.

AC ADR09337;

DT 04-NOV-2004 (first entry)

DE Human protein useful for treating neurological disease Seq 2843.

KM human; oligo-capping method; diagnostic marker; gene therapy;
 KW osteoporosis; neurological disease; Alzheimer's disease;
 KW Parkinson's disease; dementia; short memory; cancer;
 KW sense or motor function; emotional reaction; fear response; panic;
 KW osteopathic; neuroprotective; nootropic; antiparkinsonian; cyostatic;
 KW tranquiliser.

OS Homo sapiens.

PN EP1447413-A2.

PD 18-AUG-2004.

PF 12-FEB-2004; 2004EP-00003145.

PR 14-FEB-2003; 2003JP-00102207.

PR 09-MAY-2003; 2003JP-00131452.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Yamamoto J, Nishikawa T, Isomo Y, Sugiyama T, Otsuki T;

PI Wakamatsu A, Ishii S, Nagai K, Irie R;

DR WPI; 2004-583265/57.

XX N-PSDB; ADR07381.

PT New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
XX
PS Claim 1; SEQ ID NO 2843; 2686pp; English.
XX
CC This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunosay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, nociceptive, antiparkinsonian,
CC cytoskeletal and tranquilizer activities. This polypeptide is a protein
CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.
XX
SQ Sequence 401 AA:
XX
Query Match 75.6%; Score 1605; DB 8; Length 401;
Best Local Similarity 88.0%; Pred. No. 2.2e-147;
Matches 324; Conservative 11; Mismatches 33; Indels 0; Gaps 0;
XX
QY 50 VGGDLTMAAIGAGLFTSSFRHSSVAFLFMLALGVQWAILDGLSGPSPGKVIT 109
DB 34 VGGDLTMAAIGAGLFTSSFRHSSVAFLFMLALGVQWAILDGLSGPSPGKVIT 93
QY 110 LFSIMATMSALSVLSDAVLGVNLALQVWVLEVTDLGNLRVINSINFTDYMNM 169
DB 94 LFSIRLATMSAMSVLISAGAVLGRVNLALQVWVLEVTDLGNLRVINSINFTDYMNM 153
QY 170 MHIVFAAYFGLTYAKCLPRPLPREGTENDORATIPSLAMLGLFLMFRPVSNAALR 229
DB 154 RHFAVFAAYFGLTYAKCLPRPLPREGTENDORATIPSLAMLGLFLMFRPVSNAALR 213
QY 230 SPIERKAAVFNTYAAVAVSVTTAISGSSLAHPQKISKTYGHSVLPDEGVAVDPSCHLIP 289
DB 214 SPIORKAAMFNTYAAVAVSVTTAISGSSLAHPQKISKTYGHSVLPDEGVAVDPSCHLIP 273
QY 290 SPMLPIVLGLVAGLISVRGAKYLPGCCNRVLAGIPHSSIMGYNPSLGLBEIYIVLLVL 349
DB 274 SPMLAMVLGLVAGLISVRGAKYLPGCCNRVLAGIPHSSIMGYNPSLGLBEIYIVLLVL 333
QY 350 DTYGAGNGMTGFQVULSIBLSLAIVALTSGLTALLNLKIRKAPHEAKYFPDQVFWK 409
DB 334 HTWNGNGMTGFQVULSIBLSLAIVALTSGLTALLNLKIRKAPHEAKYFPDQVFWK 393
QY 410 FPHLAVGF 417
DB 394 FPHLAVGF 401
XX
RESULT 13
ADD46523
ID ADD46523 standard; protein: 422 AA.
XX
AC ADD46523;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Rat Protein NP_071950, SEQ ID NO 12204.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX
OS Rattus norvegicus.
XX Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX 01-NOV-2001; 2001US-0346382P.
XX 26-NOV-2001; 2001US-033347P.
XX
XX (GENO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M,
XX
XX WPI; 2003-268312/26.
XX GENBANK; NP_071950.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX method for identifying a compound or small molecule that regulates the
XX activity in an animal of one or more of the polypeptides given in the
XX specification, a method for identifying a compound useful in treating
XX pain and a pharmaceutical composition comprising the one or more
XX polypeptides or their antibodies. The polynucleotide or the compound that
XX modulates its activity is useful for preparing a medicament for treating
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX therapy). The sequence presented is a rat protein (described in Table 3
XX of the specification) which is differentially expressed during pain.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 422 AA:
XX
Query Match 46.7%; Score 991.5; DB 7; Length 422;
Best Local Similarity 52.1%; Pred. No. 1.4e-87;
Matches 222; Conservative 54; Mismatches 137; Indels 13; Gaps 5;
XX
QY 1 MSCGPRSVORCPPLCALTEALILLFYFTHYDASLEPOKGLVAVSYGVGGDLTMAAI 60
DB 1 MSGKPRSLRCCPLPAFGQVTFILFLYFLIGODPQADHK-FMAIYQVITQDITLVAAI 59
QY 61 GLGFLTSSFRHSSVAFLFMLALGVQWAILDGLSGPSPGKVITLPSIWL---A 116
DB 60 GFGFLTSSFRHSSVAFLFMLALGVQWITLLDVFELNVLMNMKPNFSPPLSIORA 119
QY 117 TMSALSVLISVDVAVLGVNLALQVWVLEVTDLGNLRVINSINFTDYMNMNHIVFA 176
DB 120 TISTPLLSAGAVLGVNLVOLAQVWVLEAMTGAIRVADKVFRIEDHIMVYGHVFG 179

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QY 177 AYFGITVAWMCIPKLPFEGEDND-----ORATIPBSLMLGALFLMFRPSVNSALLRSP 231
D 180 AYFGITVAWMCIPKLPFEGEDND-----ORATIPBSLMLGALFLMFRPSVNSALLRSP 238
QY 232 IERKNAVENTYYAVAVSVTTAIGSSSLAPQGIKSTYGHSAVLPBGAVDTSCHLIPSP 291
D 239 TKKNAVENTYYAVAVSVTTAIGSSSLAPQGIKSTYGHSAVLPBGAVDTSCHLIPSP 298
QY 292 WLPYVGLVAGLISVGAAXLPGCCNRVIGIPHSIMGYNFSLGLLEIITYVLVLD 351
D 299 WIMAVGLTAGLISVGAAXLPGCCNRVIGIPHSIMGYNFSLGLLEIITYVLVLD 356
QY 352 VGAGNGMIGFOVLISIGELSLAIVALTSGLLTALMLNKIRKAPHEAKYFDDQVFWKFP 411
D 357 SRPSNLMIVTQITTDVGAISFAMAMGMVGTGLTGCLLSVKWRAPHAVKYFDDQVFWKFP 416
QY 412 HLAVER 417
D 417 HLAVER 422

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RESULT 14
ADE54447
ID ADE54447 standard; protein; 422 AA.
XX

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AC ADE54447;
XX
DT 29-JAN-2004 (first entry)
XX

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DE Rat Protein NP_071950, SEQ ID NO 250.
XX

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KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX

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OS Rattus norvegicus.
XX
PN W02003016475-A2.
XX

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PD 27-FEB-2003.
XX

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PF 14-AUG-2002; 2002WO-US025765.
XX

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PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX

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PA (GHEO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX

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XX Woolf C, D'urso D, Reftor K, Costigan M;
XX

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DR WPI; 2003-268312/26.
DR GENBANK; NP_071950.
XX

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PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX

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PS Claim 1; Page; 1017p; English.
XX

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XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a
XX compound that regulates the activity of one or more of the
XX polynucleotides, a method for producing a pharmaceutical composition, a
XX

```

```

CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides that regulate the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIP0 at
CC ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 422 AA;
XX

```

```

Query Match 46.7%; Score 991.5; DB 7; Length 422;
Best Local Similarity 52.1%; Pred. No. 1.4e-87;
Matches 222; Conservative 54; Mismatches 137; Indels 13; Gaps 5;

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QY 1 MSCKYPSVQRCPLCALTLLEALILFFFTHYDASLEDDOKGLVASYGVGDITVMAAI 60
D 1 MSCKYPSVQRCPLCALTLLEALILFFFTHYDASLEDDOKGLVASYGVGDITVMAAI 59
QY 61 GLGFLTSPRRHGWSSVAFNLFWLALGVQWAILDGLSOFPSGKVVITLSIWL----A 116
D 60 GFGFLSSFRHGWSSVAFNLFWLALGVQWAILDGLSOFPSGKVVITLSIWL----A 119
QY 117 TMSALSVLISVDVAVGKVLIAQLVAVVAVLEVDLGNLRLKVISNIFNTDHYMMHIIYFA 176
D 120 TISTLEPLISAGAVGKVLVQLAVVAVLEANTPFAINADKKVRIEDHIIIMTGHVFG 179
QY 177 AYFGITVAWMCIPKLPFEGEDND-----ORATIPBSLMLGALFLMFRPSVNSALLRSP 231
D 180 AYFGITVAWMCIPKLPFEGEDND-----ORATIPBSLMLGALFLMFRPSVNSALLRSP 238
QY 232 IERKNAVENTYYAVAVSVTTAIGSSSLAPQGIKSTYGHSAVLPBGAVDTSCHLIPSP 291
D 239 TKKNAVENTYYAVAVSVTTAIGSSSLAPQGIKSTYGHSAVLPBGAVDTSCHLIPSP 298
QY 292 WLPYVGLVAGLISVGAAXLPGCCNRVIGIPHSIMGYNFSLGLLEIITYVLVLD 351
D 299 WIMAVGLTAGLISVGAAXLPGCCNRVIGIPHSIMGYNFSLGLLEIITYVLVLD 356
QY 352 VGAGNGMIGFOVLISIGELSLAIVALTSGLLTALMLNKIRKAPHEAKYFDDQVFWKFP 411
D 357 SRPSNLMIVTQITTDVGAISFAMAMGMVGTGLTGCLLSVKWRAPHAVKYFDDQVFWKFP 416
QY 412 HLAVER 417
D 417 HLAVER 422

```

```

RESULT 15
ADE54443
ID ADE54443 standard; protein; 422 AA.
XX

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AC ADE54443;
XX

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DT 29-JAN-2004 (first entry)
XX

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```

DE Rat Protein NP_071950, SEQ ID NO 246.
XX

```

```

KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX

```

```

OS Rattus norvegicus.
XX

```

```

PN W02003016475-A2.
XX

```

```

PD 27-FEB-2003.
XX

```

```

PF 14-AUG-2002; 2002WO-US025765.
XX

```


XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; NP_071950.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017p; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
XX
SQ Sequence 422 AA;
Query Match 46.7%; Score 991.5; DB 7; Length 422;
Best Local Similarity 52.1%; Pred. No. 1,4e-87;
Matches 222; Conservative 54; Mismatches 137; Indels 13; Gaps 5;
QY 1 MSCKYPRSVGRCLPLCALTEALILLFPFTHYDASLEDOKGLVASVYOGDITVMAAI 60
DB 1 MGSKYPRSLRCLPLMAFGLOVTFILFVFLIGQDPQADHK-FMALYQVYIQLTVAAL 59
QY 61 GLGFLTSSFRHSHSVAFNLFMALGVQMAILLDSQFSPSGKVITLPSITWL---A 116
DB 60 GFGFLSSFRHSHSVAFNLFMALGVQGITLLDYFLNWLDMNMIKNPSPFLSIQRA 119
QY 117 TMSALSVLISVDAVLGKVNLAQLVVMVLEVEYTDLGNLRMVISNIFNTDYNHNMHIVFA 176
DB 120 TISTLPLISAGAVLGKVNLAQLVVMVLEVEYTDLGNLRMVISNIFNTDYNHNMHIVFA 179
QY 177 AYFGLIVAMCLPKPELPEGTEDND---QRATIPSLISAMLGALFLMMFRPSVNSALLRSP 231
DB 180 AYFGLIVAMCLPKPELPEGTEDND---QRATIPSLISAMLGALFLMMFRPSVNSALLRSP 238
QY 232 IERRNAVENTYVAVSVVTAIAGSSLAHPOGKISKTYGSAVLPRGVAVDTSCHLPSR 291
DB 239 TKKNAVENTYVAVSVVTAIAGSSLAHPOGKISKTYGSAVLPRGVAVDTSCHLPSR 298
QY 292 WLPVIVGLVAGLISVRGAKYLPCCNRLVGI PHSSINGYNFSLGLLEELIYIVLVLDIT 351

DB 299 WIMVVLGTAGLISIMWAKCPQVCLSDLLNP---SGIHVTFGLRGLGALTYCTHIAE 356
QY 352 VGANGMIGQVQLISIGELSLAIVIALTSGLLALLNLKIRKAPHEAKTFFDQVFWKFP 411
DB 357 SRPSNLWIVQTITDVGALSFMAMGMVGTILTGCLLSVYKWRAPHAVKYFDQAFWEFP 416
QY 412 HLAVER 417
DB 417 HLAVER 422

Search completed: March 24, 2005, 13:16:41
Job time : 168 secs

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OM protein - protein search, using sw model

Run on: March 24, 2005, 13:17:10 ; Search time 142 Seconds
(without alignments)
972.317 Million cell updates/sec

Title: CAC07879
Perfect score: 2124
Sequence: 1 MSCKYRSVGRCLPLCALTL.....EAKYFDQVWKRPFLAVGF 417

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues
Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match Length	ID	Description
1	521	24.5	459 15 US-10-074-978A-246	Sequence 246, App
2	497	23.4	479 9 US-09-949-145-3	Sequence 3, Appl1
3	497	23.4	479 15 US-10-074-978A-244	Sequence 244, App
4	490	23.1	445 15 US-10-074-978A-42	Sequence 42, Appl
5	488.5	23.0	498 9 US-09-949-145-4	Sequence 4, Appl1
6	488.5	23.0	498 15 US-10-074-978A-245	Sequence 245, App
7	486	22.9	467 15 US-10-074-978A-247	Sequence 247, Appl
8	480.5	22.6	455 15 US-10-190-115-58	Sequence 58, Appl
9	480.5	22.6	455 15 US-10-369-072-58	Sequence 59, Appl
10	477	22.5	458 15 US-10-190-115-59	Sequence 59, Appl
11	477	22.5	458 15 US-10-369-072-59	Sequence 59, Appl
12	476	22.4	324 16 US-10-408-765A-1089	Sequence 1089, Ap
13	472.5	22.2	458 15 US-10-190-115-57	Sequence 57, Appl

14	472.5	22.2	458 15 US-10-369-072-57	Sequence 57, Appl
15	466.5	22.0	458 15 US-10-190-115-55	Sequence 55, Appl
16	466.5	22.0	458 15 US-10-369-072-55	Sequence 55, Appl
17	465.5	21.9	458 15 US-10-190-115-56	Sequence 56, Appl
18	465.5	21.9	458 15 US-10-369-072-56	Sequence 56, Appl
19	464	21.8	458 15 US-10-074-978A-248	Sequence 248, App
20	444	20.9	458 15 US-10-074-978A-249	Sequence 249, App
21	374	17.6	448 15 US-10-190-115-22	Sequence 22, Appl
22	374	17.6	448 15 US-10-369-072-22	Sequence 22, Appl
23	302	14.2	326 15 US-10-264-237-2412	Sequence 2412, Ap
24	257	12.1	54 9 US-09-864-761-34840	Sequence 34840, A
25	247.5	11.7	395 15 US-10-190-115-100	Sequence 100, App
26	247.5	11.7	395 15 US-10-369-072-100	Sequence 100, App
27	220	10.4	373 15 US-10-074-978A-250	Sequence 250, App
28	202	9.5	145 14 US-10-012-543-438	Sequence 438, App
29	202	9.5	145 14 US-10-113-123-438	Sequence 438, App
30	164.5	7.7	459 9 US-09-795-693-32	Sequence 32, Appl
31	164.5	7.7	459 14 US-10-156-233-32	Sequence 32, Appl
32	164.5	7.7	459 14 US-10-199-485-32	Sequence 437, App
33	142	6.7	308 14 US-10-012-543-437	Sequence 437, App
34	142	6.7	308 14 US-10-115-123-437	Sequence 437, App
35	124.5	5.9	447 15 US-10-282-122A-52221	Sequence 52221, A
36	122	5.7	523 15 US-10-282-122A-52841	Sequence 62841, A
37	120	5.6	662 11 US-09-864-408A-1672	Sequence 1672, Ap
38	120	5.6	537 15 US-10-282-122A-64691	Sequence 64691, A
39	119.5	5.6	424 15 US-10-369-493-1146	Sequence 1146, Ap
40	119.5	5.6	891 15 US-10-282-122A-77590	Sequence 77590, A
41	117.5	5.5	612 15 US-10-282-122A-58936	Sequence 58936, A
42	114	5.4	529 14 US-10-156-761-12058	Sequence 12058, A
43	114	5.4	801 15 US-10-282-122A-70493	Sequence 70493, A
44	113.5	5.3	440 15 US-10-282-122A-59941	Sequence 59941, A
45	113.5	5.3	601 15 US-10-369-493-11844	Sequence 11844, A

ALIGNMENTS

RESULT 1
US-10-074-978A-246
; Sequence 246, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Lette, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Patuturajan, Weera
; APPLICANT: Bialock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vernet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkete, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A111e
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shiomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John

```
/ APPLICANT: Smithsonian, Glenda
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-269
/ CURRENT APPLICATION NUMBER: US/10/074,978A
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: 60/268,221
/ PRIOR FILING DATE: 2001-02-12
/ PRIOR APPLICATION NUMBER: 60/335,109
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: 60/312,284
/ PRIOR FILING DATE: 2001-08-14
/ PRIOR APPLICATION NUMBER: 60/268,496
/ PRIOR FILING DATE: 2001-02-13
/ PRIOR APPLICATION NUMBER: 60/276,703
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/330,293
/ PRIOR FILING DATE: 2001-10-18
/ PRIOR APPLICATION NUMBER: 60/322,127
/ PRIOR FILING DATE: 2001-11-21
/ PRIOR APPLICATION NUMBER: 60/280,899
/ PRIOR FILING DATE: 2001-04-02
/ PRIOR APPLICATION NUMBER: 60/310,797
/ PRIOR FILING DATE: 2001-08-08
/ PRIOR APPLICATION NUMBER: 60/268,646
/ PRIOR FILING DATE: 2001-02-14
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 547
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 246
/ LENGTH: 459
/ TYPE: PRT
/ ORGANISM: Bos taurus
US-10-074-978A-246

Query Match
Best Local Similarity 24.5%; Score 521; DB 15; Length 459;
Matches 138; Conservative 75; Mismatches 177; Indels 48; Gaps 10;

13 LPLCALTEALILFFFTHYDASLED-----OKGLVAS-----YQVGODLTVM 57
11 LPLCALTEALILFFFTHYDASLED-----OKGLVAS-----YQVGODLTVM 57
58 AALGGLTSSFRHSSVAENLFMLALGVOMAILLDGFLSOPPSKVVITLFSITLAT 117
71 IFVGGFLMTFLQRYGSSVGFN-FLAAGIOMAILLQWMLQSGDGRYIIVDLNLINAD 129
118 MSALSVLSVAVYGVKVNLAQVVMVIVETDGLNLMVINSIFNTDYHNMNHIIYFAA 177
130 FCVGSVCVAFGAVGVKVSPOVLLIMTLFOVTLFVSINEYIILNLELVDSGSMTHAFGA 189
178 YFGITVAMCLPKPLPEGEDNDQKATIPSLSAMIGALFLMFRPSVNSALLRSPIERKVA 237
190 YFGITVAMILYRPMHLHSKERSQSTYHSDLPAMIGTLFLMWPSPFNSAISNHDQHRRA 249
238 VENTYVAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIYL 297
250 AINTYCSLAACVLTSSALHKKGLDMVHIQNNLTLAGVGLGYAEIEMVLPFSGSLII 309
298 GLVAGLISVGAKYL-----PGCCNRVLGIPIHSSIMGVNFSLL 335
310 GFVGGITVSTLGFVYLLPFLSRLHIQDTGCVNHLHGIPGIIIGIAGAVASIA--NIDLY 367
336 GLLEELIYIVLVLDIVGAGNMIG-FOVLLSIGELISAIIVALTSGILTALLNLNKI-R 393
368 G-BEGLAVAFGIRSKLNMSPNNQGRFGA---AGLFSILMALVGVGIVGLIRLPFWG 422
394 KAPHEAKYFPDOVFWKFP 411
423 QAPDE-NCFEDAVYWEIP 439
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RESULT 2
US-09-949-145-3

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/ Sequence 3, Application US/09949145
/ Patent No. US20020055622A1
/ GENERAL INFORMATION:
/ APPLICANT: New York Blood Center
/ TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glycoi
/ FILE REFERENCE: Docetel 454-31
/ CURRENT APPLICATION NUMBER: US/09/949,145
/ PRIOR FILING DATE: 2001-09-07
/ PRIOR APPLICATION NUMBER: US 60/230660
/ PRIOR FILING DATE: 2000-09-07
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 479
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-949-145-3

Query Match
Best Local Similarity 23.4%; Score 497; DB 9; Length 479;
Matches 129; Conservative 77; Mismatches 183; Indels 50; Gaps 8;

13 LPLCALTEALILFFFTHYD-----ASLEDKG-LVASVQVGODLTVM 58
11 LPLCALTEALILFFFTHYD-----ASLEDKG-LVASVQVGODLTVM 58
59 AALGGLTSSFRHSSVAENLFMLALGVOMAILLDGFLSOPPSKVVITLFSITLATM 118
71 IFVGGFLMTFLQRYGSSVGFN-FLAAGIOMAILLQWMLQSGDGRYIIVDLNLINAD 130
119 SALSVLSVAVYGVKVNLAQVVMVIVETDGLNLMVINSIFNTDYHNMNHIIYFAAY 178
131 CVASVCVAFGAVGVKVSPOVLLIMTLFOVTLFVANEFLILNLKVKAGSGMTHTTFCAG 190
179 YFGITVAMCLPKPLPEGEDNDQKATIPSLSAMIGALFLMFRPSVNSALLRSPIERKVA 238
191 FGLTVTRILYRNLHRSKERSQSTYHSDLPAMIGTLFLMWPSPFNSAISNHDQHRRA 250
239 FNTYVAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLIPSPMLPIYL 298
251 INTYCSLAACVLTSSALHKKGLDMVHIQNNLTLAGVGLGYAEIEMVLPFSGSLII 310
299 LVAGLISVGAKYL-----PGCC--NRVLGIPIHSSIMGVNFSLLGLEELIYIVL 346
311 FVCGIISTLGFVYLLPFLSRLHIQDTGCVNHLHGIP-----GIIGIAGAVASIA 361
347 LVLDIVGAGNMIG-----GF-----QVLLSIGELISAIIVALTSGILTALLNLNKI 392
362 ASLEVYVGK-EGIVHSFPDQGFNGDMTARTQKFOIYGLVTLMALMGIIIVGLIRLPF 420
393 KAPHEAKYFPDOVFWKFP 411
421 WQPSDENCFEDAVYWEIP 439

RESULT 3
US-10-074-978A-244
/ Sequence 244, Application US/10074978A
/ Publication No. US20040010119A1
/ GENERAL INFORMATION:
/ APPLICANT: Leite, Mario
/ APPLICANT: Spytek, Kimberly A
/ APPLICANT: Guo, Xiaojia (Sasha)
/ APPLICANT: Fernandes, Elma
/ APPLICANT: Li, Li
/ APPLICANT: Kekuda, Ramesh
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Caeman, Scacie
/ APPLICANT: Boldog, Ferenc
/ APPLICANT: Paturajan, Meera
/ APPLICANT: Blalock, Angela
/ APPLICANT: Ballinger, Robert
/ APPLICANT: Verneet, Corine
```

```

: APPLICANT: Tchernev, Velizar T
: APPLICANT: Malyankar, Uriel M
: APPLICANT: Gusev, Vladimir
: APPLICANT: Rastelli, Luca
: APPLICANT: Mezes, Peter S
: APPLICANT: Ellerman, Karen
: APPLICANT: Heyes, Melvin P
: APPLICANT: Herrman, John
: APPLICANT: Pena, Carol E A
: APPLICANT: Shinkete, Richard A
: APPLICANT: Taupier Jr, Raymond J
: APPLICANT: Moore, No. US20040010119A11le
: APPLICANT: Shenoy, Suresh
: APPLICANT: Edinger, Shlomit
: APPLICANT: Gunther, Erik
: APPLICANT: Stone, Dave
: APPLICANT: Mallet, Isabelle
: APPLICANT: Peyman, John
: APPLICANT: Smlthson, Glenda
: TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: 21402-269
: CURRENT APPLICATION NUMBER: US/10/074,978A
: CURRENT FILING DATE: 2003-01-07
: PRIOR APPLICATION NUMBER: 60/268,221
: PRIOR FILING DATE: 2001-02-12
: PRIOR APPLICATION NUMBER: 60/335,109
: PRIOR FILING DATE: 2001-10-31
: PRIOR APPLICATION NUMBER: 60/312,284
: PRIOR FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: 60/268,496
: PRIOR FILING DATE: 2001-02-13
: PRIOR APPLICATION NUMBER: 60/276,703
: PRIOR FILING DATE: 2001-03-16
: PRIOR APPLICATION NUMBER: 60/330,293
: PRIOR FILING DATE: 2001-10-18
: PRIOR APPLICATION NUMBER: 60/322,127
: PRIOR FILING DATE: 2001-11-21
: PRIOR APPLICATION NUMBER: 60/280,899
: PRIOR FILING DATE: 2001-04-02
: PRIOR APPLICATION NUMBER: 60/310,797
: PRIOR FILING DATE: 2001-08-08
: PRIOR APPLICATION NUMBER: 60/268,646
: PRIOR FILING DATE: 2001-02-14
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 547
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 244
: LENGTH: 479
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-10-074-978A-244

Query Match      23.4%; Score 497; DB 15; Length 479;
Best Local Similarity 29.4%; Pred. No. 1.3e-37;
Matches 129; Conservative 77; Mismatches 183; Indels 50; Gaps 8;

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DB      11 LPLTCLLOVIMVILFGVFRYPDEADAHMWSERTHKNLSMENEFFYRYPSPFDVHMV 70
QY      59 AIGGLFSSPFRHSWSVAFNLFMLALGVOMAILLGLSOPSGKVITLPSIWTATM 118
DB      71 FVGEGFLMTLQKGFSAVGFNFIILAFGIOMALLMGWMEHFLDRIYVGEVLINADF 130
QY      119 SALSVLISVDALVKVLAOLVWVLEVTDLGNLRVINSIFNTDYHMMMHIIYVEAY 178
DB      131 CVASVCAFAVGLVKVSPILQILMTFQVTLFAVNEFILNLTLKVKDAGSMTIHTFGAY 190
QY      179 FGLTVANCLPKRPEEGEDNDQKATISLSMGLALTLMPRESVNSALRSPERKNAV 238
DB      191 FGLTVTRILVARNLEQSKERONSYYQSDLFAMITGLFLMWTSPFNSAISYHGDSORAA 250
QY      239 FNTYVAVAVSVTAISGSSLAHPQKISKTYGSAVLPEGVAVDTSCHLTPSPWLPIVLG 298
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DB      251 INTYGLACVLTSAVIASSHLHKKGLDWHIGNATLAGVANAGTAEMLMWRYGALITG 310
QY      299 LVAGLISVRGAKYL-----PCCC--NRVLGIPHSSIMGYNSSLGLEBIYIVL 346
DB      311 FVCGIISTLGFVYLTLPFLBSRLHIPTCGINNHLGIP-----GIIGIYCAVTPAAS 361
QY      347 LVLDIVGAGNGM-----GF-----QVLLSIBLSAIVIALTSGLLTALLNLKI 392
DB      362 ASLEVVYK-EGLVHSPDFQGFNDMTARTQKFOITGLVTLAMALMGIIIVGLIRLPF 420
QY      393 RKAPHEAKYFDDQVFWKFP 411
DB      421 WQGPSPDENCEDADVWEMP 439

RESULT 4
US-10-074-978A-42
: Sequence 42, Application US/10074978A
: Publication No. US20040010119A1
: GENERAL INFORMATION:
: APPLICANT: Leite, Mario
: APPLICANT: Spytek, Kimberly A
: APPLICANT: Guo, Xiaojia (Sasha)
: APPLICANT: Fernandes, Elma
: APPLICANT: Li, Li
: APPLICANT: Kekuda, Ramesh
: APPLICANT: Liu, Xiaohong
: APPLICANT: Casman, Stacie
: APPLICANT: Boldog, Ferenc
: APPLICANT: Paturajan, Meera
: APPLICANT: Bialock, Angela
: APPLICANT: Ballinger, Robert
: APPLICANT: Verneil, Corine
: APPLICANT: Tchernev, Velizar T
: APPLICANT: Malyankar, Uriel M
: APPLICANT: Gusev, Vladimir
: APPLICANT: Rastelli, Luca
: APPLICANT: Mezes, Peter S
: APPLICANT: Ellerman, Karen
: APPLICANT: Heyes, Melvin P
: APPLICANT: Herrman, John
: APPLICANT: Pena, Carol E A
: APPLICANT: Shinkete, Richard A
: APPLICANT: Taupier Jr, Raymond J
: APPLICANT: Moore, No. US20040010119A11le
: APPLICANT: Shenoy, Suresh
: APPLICANT: Edinger, Shlomit
: APPLICANT: Gunther, Erik
: APPLICANT: Stone, Dave
: APPLICANT: Mallet, Isabelle
: APPLICANT: Peyman, John
: APPLICANT: Smlthson, Glenda
: TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
: FILE REFERENCE: 21402-269
: CURRENT APPLICATION NUMBER: US/10/074,978A
: CURRENT FILING DATE: 2003-01-07
: PRIOR APPLICATION NUMBER: 60/268,221
: PRIOR FILING DATE: 2001-02-12
: PRIOR APPLICATION NUMBER: 60/335,109
: PRIOR FILING DATE: 2001-10-31
: PRIOR APPLICATION NUMBER: 60/312,284
: PRIOR FILING DATE: 2001-08-14
: PRIOR APPLICATION NUMBER: 60/268,496
: PRIOR FILING DATE: 2001-02-13
: PRIOR APPLICATION NUMBER: 60/276,703
: PRIOR FILING DATE: 2001-03-16
: PRIOR APPLICATION NUMBER: 60/310,797
: PRIOR FILING DATE: 2001-08-08
: PRIOR APPLICATION NUMBER: 60/268,646
: PRIOR FILING DATE: 2001-02-14
: PRIOR APPLICATION NUMBER: 60/280,899
: PRIOR FILING DATE: 2001-04-02
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; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 42
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-074-978A-42

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Query Match      23.1%; Score 490; DB 15; Length 445;
Best Local Similarity 29.3%; Pred. No. 5,5e-37;
Matches 128; Conservative 77; Mismatches 182; Indels 50; Gaps 8;

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QY 13 LPLCALTEALALLFFFTTHYD-----ASLEDOKG-LVASQVQODLTWMA 58
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D 11 LPLTCLLOVIMVILFVGVRVYDFEADAHMWSERTKNSIDWENEFYRPSFQDVHVMV 70
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 59 AIGLGLTSSFRHSSWSVAFLFMALGVOMAILDGLSQPSGKVITLFSIWLATM 118
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D 71 FVGFGLMTFLQRYGSAVGFNPLAARFQIALMQGFHFLQDRYIVGVENLINDP 130
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 119 SALSVLISVDAYLGKYNLAQIVVMVLVEYTDLGNLRMVISNIFNTDYHNNMHIVFPAAY 178
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 131 CVASVCVAGAVLGKSPQOLIMTFEYVTLFVAVNEFILMLKVKDAGSGMTIHTFPA 190
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 179 FGLTVAMCLPKPLPEGTEDNDQRATIPSLSAMLGLFLMPPSPNSALLSPERKNAV 238
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 191 FGLTVIRILYRNLDQSKRQNSVYQSDLFPMITGTLFMTWPSFNSAISYHGDSDHAA 250
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 239 FNTTYAVAVSVVTAISGSLAHPOGKISKTYGHSVLPBGVAVDTSCHLIPSPMLPTVLG 298
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D 251 INTYGSACVLTVAISSALHKKGLDMVHIQNATLAGVAVGAEMMLTPGALIT 310
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QY 239 LVAGLISYRGAKYL-----PGCC--NRVLGIPHSIMGNISLGLLEIYIVL 346
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D 311 FVCGIISTLGFVYLPPLIESRLHIQDTGGINLHGIP-----GIIGIVGAVTAAS 361
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 347 LVLDTVGANGMI-----GF-----QVLLSIGELSLAIVALTSGLLTLNLK 392
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D 362 ASLEVYGR-EGLVHSFDFQGFNGDMTARTQCKPQIYGLVTLAMALMGIIIVGLILKLP 420
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QY 393 RKAPHEAKYEDDOYFWK 409
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RESULT 5
US-09-949-145-4
; Sequence 4, Application US/09949145
; Patent No. US20020055622A1
; GENERAL INFORMATION:
; APPLICANT: New York Blood Center
; TITLE OF INVENTION: Mammalian No. US20020055622A1-erythroid Rh Type C Genes and Glyco
; FILE REFERENCE: Docket 454-31
; CURRENT APPLICATION NUMBER: US/09/949,145
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/230660
; PRIOR FILING DATE: 2000-09-07
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 4
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-949-145-4

```

```

Query Match      23.0%; Score 488.5; DB 9; Length 498;
Best Local Similarity 28.0%; Pred. No. 8,9e-37;
Matches 120; Conservative 86; Mismatches 191; Indels 31; Gaps 4;

```

```

QY 13 LPLCALTEALALLFFFTTHYD-----LEDOKGLVAS-----YQVQODLTWMA 57
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 11 LPLTCLLOVIMVILFVGVRVYDIQADAHMWLEKRRKNISSDVWENEFYRPSFQDVHVM 70
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 58 AIGLGLTSSFRHSSWSVAFLFMALGVOMAILDGLSQPSGKVITLFSIWLATM 117
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 71 FVGFGLMTFLQRYGSAVGFNPLAARFQIALMQGFHFLQDRYIVGVENLINDP 130
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 118 MSALSVLISVDAYLGKYNLAQIVVMVLVEYTDLGNLRMVISNIFNTDYHNNMHIVFPA 177
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 131 FCVASCCVAGAVLGKSPQOLIMTFEYVTLFVAVNEFILMLKVKDAGSGMTIHTFPA 190
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 178 FGLTVAMCLPKPLPEGTEDNDQRATIPSLSAMLGLFLMPPSPNSALLSPERKNA 237
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 191 FGLTVIRILYRNLDQSKRQNSVYHSDLFPMITGTLFMTWPSFNSASHGDAQHRA 250
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 238 FNTTYAVAVSVVTAISGSLAHPOGKISKTYGHSVLPBGVAVDTSCHLIPSPMLPTVL 297
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 251 ALNTYLSLASVLTVAISSIVHKKGLDMVHIQNATLAGVAVGAEMMLTPGALIT 310
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 298 GLVAGLISYRGAKYLPGCCNRVLGIPHSIMGNISLGLLEIYIVL----- 347
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 311 GFPCGIFSTLGFAYLPLPLIESRLHIQDTGGINLHGIPGIVGAVTAAYSSPDYGE 370
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 348 --VLDTVGANGMIGF-----QVLLSIGELSLAIVALTSGLLTLNLKIRKAPHEAKY 401
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 371 PGIVHSFGFSGYKMDNKRQSGQIFGLLSLALMVLGIIIVGPIFLKPFMGQADLNC 430
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
QY 402 FDDOYFWK 409
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
D 431 FEDSIYWE 438
| | | | | : : : : : | | | | | : : : : : | | | | | : : : : :

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```

RESULT 6
US-10-074-978A-245
; Sequence 245, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Rameesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boleog, Ferenc
; APPLICANT: Patuturajan, Meera
; APPLICANT: Blalock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Verneer, Corine
; APPLICANT: Tcherenev, Velizar T
; APPLICANT: Maljankar, Uriel M
; APPLICANT: Gusev, Vladimyr
; APPLICANT: Raetelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herrman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shinkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A111e
; APPLICANT: Shenoy, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Millet, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smithson, Glenda
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269

```

```

; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 245
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Mus musculus
; US-10-074-978A-245
```

```

Query Match      23.0%; Score 488.5; DB 15; Length 498;
Best Local Similarity 28.0%; Pred. No. 8.9e-37;
Matches 120; Conservative 86; Mismatches 191; Indels 31; Gaps 4;
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```

QY 13 LPLCALTLLEAALLLFFFTTHYDAS-----LEDDKGLVAS-----YGVGQDLTVM 57
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 11 LPLTCLLYTMTVMVLFGEVFRYDQLQADAHMMLLEKKRKNISDVENEFRYRPSFDVHAM 70
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 58 AAIIGLGLTSSFRHRSSVAENFMIALGVQMAILLDGLSQPSPGKVVITLFSIVLAT 117
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 71 VFGVFGFLMTFLQRYGFSAVGFNLLAFCGIOMALLMGWFHYPEEGHIVLSVENITQAD 130
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 118 MSALSVLISVDAYLGVKNLAQVLVTVLVETVDLGNLNVISNIENTYHNMWHIYVEAA 177
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 131 FCVAASSVAFGAVALGVKVSFMOQLMTFTFOVTLFTVNEPILNLEAKDAGGSMTHTEGA 190
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 178 YFGITVAMCLPKPLREGTEBNDQRTTIPSLSAMLGALFLMFRPSVNSALIRSPIERKNA 237
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 191 YFGITVWILYRKLDQSKQROSSVYHSDLEFAMIGTIFLWMTYWSFBSASSFHDDAQRHA 250
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 238 VENTYVAVASVTAIGSSILAPQOKISKTYGSAVLPEGVAVDTSCHLIPSPWLDIVL 297
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 251 ALNTYVLSLAASVLTVTVSSIVHKKGKLDVWHIQNATLAGGVGTAAEMMLTPYGALIV 310
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 298 GIVAGLISVGAAYLPGCCNRVILGIPIHSSIMGNFSLGLLEIYIVLV----- 347
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 311 GFPGGISTIGFAYLTPLESRLRIQDTGCHNHGIPGIIIGIVGVTAAVSPDYGE 370
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 348 --VLDTVAGANGMIGF----QVLISIGELSLAIVIALTGLTALLNLKIRKAPHEAKY 401
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 371 PGIVHSFGFSYKMDMKRMQGRSQIFGLLSLMAVLCGIIIVGFIILKLPWQGAADENC 430
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY 402 FDDOVFWK 409
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 431 FEDSIYWE 438
```

```

RESULT 7
US-10-074-978A-247
; Sequence 247, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Rima
; APPLICANT: Li, Li
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Liu, Xiaohong
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ferenc
; APPLICANT: Faturajan, Meera
; APPLICANT: Bialock, Angela
; APPLICANT: Ballinger, Robert
; APPLICANT: Vermet, Corine
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Gusev, Vladimir
; APPLICANT: Rastelli, Luca
; APPLICANT: Mezes, Peter S
; APPLICANT: Ellerman, Karen
; APPLICANT: Heyes, Melvin P
; APPLICANT: Herman, John
; APPLICANT: Pena, Carol E A
; APPLICANT: Shimkets, Richard A
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Moore, No. US20040010119A111le
; APPLICANT: Sheno, Suresh
; APPLICANT: Edinger, Shlomit
; APPLICANT: Gunther, Erik
; APPLICANT: Stone, Dave
; APPLICANT: Miller, Isabelle
; APPLICANT: Peyman, John
; APPLICANT: Smitheon, Glenda
; TITLE OR INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-269
; CURRENT APPLICATION NUMBER: US/10/074,978A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: 60/268,221
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/335,109
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 60/312,284
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/268,496
; PRIOR FILING DATE: 2001-02-13
; PRIOR APPLICATION NUMBER: 60/276,703
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/330,293
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/322,127
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/280,899
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/310,797
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/268,646
; PRIOR FILING DATE: 2001-02-14
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 247
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Oryzocetolagus cuniculus
; US-10-074-978A-247
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Query Match      22.9%; Score 486; DB 15; Length 467;
Best Local Similarity 29.1%; Pred. No. 1.4e-36;
Matches 123; Conservative 82; Mismatches 192; Indels 26; Gaps 5;
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```

QY 13 LPLCALTLLEAALLLFFFTTHY--DA-----SLEDKGLVAS-----YGVGQDLTVM 57
   |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 11 LPLTCLLYEAMVVLFLGVRYSPDADSSWSNKRKNITSLENEFYRPSFDVHAM 70
```


APPLICANT: Burgess, Catherine E
APPLICANT: Shimkets, Richard
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: No. US20040014081a1el Proteins and Nucleic Acids Encoding Same
FILE REFERENCE: 21402-050 CON2
CURRENT APPLICATION NUMBER: US/10/369, 072
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: 10/174,372
PRIOR FILING DATE: 2002-06-17
PRIOR APPLICATION NUMBER: 09/898,994
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,585
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/218,992
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 455
TYPE: PRT
ORGANISM: Mus musculus
US-10-369-072-58

Query Match 22.6%; Score 480.5; DB 15; Length 455;
Best Local Similarity 30.3%; Pred. No. 4,4e-36;
Matches 135; Conservative 72; Mismatches 189; Indels 49; Gaps 7;

4 KYRPSVORCLPLCALTEALILLFYFPTHY----DASL-----EDQGLVASVGVQ 52
3 RVRHRRLVLPCLCLFGATALLFAIFVRYNHETDALMHGNSVNDNEFFRYPSFQ 62
53 DLTMAAIGGLTSSRRHSMSVARNLPMALGVOMAILLDGFLSQFPGKAVITLFS 112
63 DVHVMVFVGGFLWVFLQRYGFSVGGFTFLVASLTLQWATLLQGLHSFHGHITHGVES 122
113 IWLATMSALSVLISVDVAVLQVLAQVVMVVLVEVTDLGNLRVVISNIFNTDYMNMWHI 172
123 LINDPFGAGVNLISFGAVLGKTGPAQLIMALLAVLFSVNEFTLLSLGVRDAGGSMTI 182
173 YVFAAYFGLTVAMWCLPKPLPEGTEDNDORATIPSLAMTALFLIMFRPSVNSALLSPI 232
183 HTFGAYFGLFSLRVLYRSQLEKSRHOSVYNSDLPAMIGITIFLMVFPSPNSAPFALGD 242
233 ERKRAVNTTYAAVAVSVVTAISGSSLAHPQCKISKITGSHAVLPEGVAVDISCHLISPM 292
243 GQHRVTNTYTSLSLSTSLFALSALVSGDRDLDMVHQNALAGVVVGTSSMMLTPTF 302
293 LPIVLGLVAGLISVRGAKY-----LEPGC--NRVLGI PRASSINGVNFSLGLLEE 340
303 GALAAGLACTAGVSTLGYKFFPILESRFKLDOTGCVINLHMP-----GVILGA 350
341 IYIVLVLLDVTGA-GNGMIGFOVLLSIGELIS-----LAIVALTSGLLTAL 386
351 ILGVVVALATHEAYGGLQGVFPLIAKGQRSAISOAVYQFGMFTVLVFAVSGSLGGL 410
367 LTNKIRKAPHEAKYPPDOVFWKFP 411
411 LRLRLPDSPPDSQCFEDQVYWEVP 435

RESULT 10
US-10-190-115-59

Sequence 59, Application US/10190115
Publication No. US20030207394A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, John P. II
APPLICANT: Boldog, Ferenc L.
APPLICANT: Burgess, Catherine E.
APPLICANT: Casman, Stacie J.
APPLICANT: Grosee, William M.
APPLICANT: Gusev, Vladimir Y.
APPLICANT: Ji, Weizhen
APPLICANT: Lepley, Denise M.
APPLICANT: Liu, Xiaohong
APPLICANT: Merick, Amanda J.
APPLICANT: Padigaru, Muralidhara
APPLICANT: Patturajan, Meera
APPLICANT: Rastelli, Luca
APPLICANT: Shen, Lei
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkets, Richard A.
APPLICANT: Spaderna, Steven K.
APPLICANT: Spytek, Kimberly A.
APPLICANT: Szekeres, Edward S. Jr.
APPLICANT: Taupier, Raymond J. Jr.
APPLICANT: Tchernev, Velizar T.
APPLICANT: Zernhusen, Bryan D.
APPLICANT: Voss, Edward Z.
TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
FILE REFERENCE: 21402-050 CIP
CURRENT APPLICATION NUMBER: US/10/190,115
CURRENT FILING DATE: 2003-02-10
PRIOR APPLICATION NUMBER: 60/303,168
PRIOR FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: 60/368,996
PRIOR FILING DATE: 2002-04-01
PRIOR APPLICATION NUMBER: 60/386,816
PRIOR FILING DATE: 2002-06-07
PRIOR APPLICATION NUMBER: 60/215,854
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,856
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/215,902
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 60/216,586
PRIOR FILING DATE: 2001-07-07
PRIOR APPLICATION NUMBER: 60/216,722
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/218,622
PRIOR FILING DATE: 2000-07-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Curoseq1ist version 0.1
SEQ ID NO 59
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
US-10-190-115-59

Query Match 22.5%; Score 477; DB 15; Length 458;
Best Local Similarity 29.8%; Pred. No. 9,4e-36;
Matches 130; Conservative 75; Mismatches 203; Indels 28; Gaps 4;

4 KYRPSV---ORCLPLCALTEALILLFYFTHYDASL-----DQKGLVASVQ 49
3 KSPRRVAVGRLLPLCLLFGATALLFAIFVRDQTDALMHGNSVNDNEFFRYFP 62
50 VGDLTMAAIGGLTSSRRHSMSVARNLPMALGVOMAILLDGFLSQFPGKAVIT 109
63 SFQDVHVMVFVGGFLWVFLQRYGYSLGFTFLGAPALQWATLLQGLHSFHGHITHG 122

```

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;
; LENGTH: 458
;
; TYPE: PRT
;
; ORGANISM: Oryctolagus cuniculus
US-10-369-072-59

```

matches 130; Conservative 75; Mismatches 203; Indels 28; Gaps 4;

QNCUFCCHILDEAALLLEFFELHYDASLE-----DQKGLVASYQ 49

50 VAGNDI TUMATIGI CEI MCEBBDUWUCUWU WU WU " " SUEWU I " "

63 SFQDVHAMVFVGEGFLMVFLQRYGYSSLGFTFLLGAFALQWATLVQGFLLHSFHGGHIHV 122

169

170 MHTVEAAVEGI TIVANCI RYRI DECTEDYDOD...TINAR OIVU 2000

183 MTHTFGAYFGLVSRVLYRPHLEKSQHRQGSVYHSDLFAMIGTIFLWIFWPSFNSATTS 242

[illegible]

290 SPWLPVTJGI VAGITSVBCKRYI BCCCNBYI CTVICSTMCNRYI : CTVICSTMCNRYI

SECRET

363 TTHA YGDGLQSVFPLIAEGORSATSOAIYOLEGI,SVTTI,FA SAGCVI,CGI,ITRPERDY 433

396 PHEAKYFDDQVFWKFP 411

423 PPDSQCYEDQMCEVP 438

SULT 12
12.10.10

Sequence 1005, Application US/10408765A
Publication No. US20040101874A1

APPLICANT: Ghosh, Soumitra S.
APPLICANT: Faby, Eoin D

APPLICANT: Gibson, Bradford W.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088 46E

CURRENT FILING DATE: 2003-04-04

EQ ID NO 1089

TYPE: PRT
ORGANISM: Homo sapiens

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[illegible]

Matches 112; Conservative 62; Mismatches 124; Indels 12; Gaps 3;

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QY 14 PLCAITLLEAAILLFYFFTHY--DASLEDQGLVASYQVG-----ODLTWMAAIGL 62
D 6 PLMAIVEIMIVLFGFVEYETDQTVLEQNIKRPIDMGFFFLYPLFDVYHMIYVGF 65
QY 63 GFLTSSFRHSHSSVAFNLFMLALGVQMAILLDGLFSLQFPGSKVITLFSIMLATMSALS 122
D 66 GFLMTFLPKYGFSSVGINLVAALGLQWGTIVGIL-QSQGQKFNIGIKMMINADFSAAAT 124
QY 123 VLISVDVAVLGNVLAQVVMVVLVEVTDLGNLRMTVINSIFNDYHMMNHIVFAAYFGLT 162
D 125 VLISFGAVLGTSTPTQIMITLIVFFPAHNEYVSELPKASDYGASVTHAFAGYFGLA 184
QY 183 VAWCLPKPLPEGTENDQORATIPSLSAMLGAFLMFRPSVNSALLRSPIERKNAVENTY 242
D 185 VAGLTVSGLRKGHENESAYSDLPFAMIGTLFLMFRPSNSAIAERGDQCRALVNTY 244
QY 243 YAAVAVSVTAISGSSLAHPQGIKSKTYGHSAYLPEGVAVDTSCHLIPSPMLPIVLGLVAG 302
D 245 FSLAACVLTAFASFSLVEHRRGKLMNVH1QNATLAGVAVGTCDMAIHPFGSMIIGSIAG 304
QY 303 LISVRGAKYL 312
D 305 MVSVLGYKFL 314
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RESULT 13

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US-10-190-115-57
; Sequence 57, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alabrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grose, William M.
; APPLICANT: Gusev, Vladimr Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Paturajan, Meera
; APPLICANT: Raestelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Shinkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR APPLICATION NUMBER: 60/303,168
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/368,996
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: 60/366,816
; PRIOR FILING DATE: 2002-06-07
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585,
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2001-07-07
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; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Curaseq1ist version 0.1
; SEQ ID NO 57
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-57
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Query Match 22.2%; Score 472.5; DB 15; Length 458;
Best Local Similarity 28.9%; Pred. No. 2.5e-35;
Matches 125; Conservative 73; Mismatches 193; Indels 41; Gaps 4;
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QY 13 LPLCALITLLEAAILLFYFFTHY-----DASL-----EDQGLVASYQVGQDLTVMAAIG 61
D 15 LPLCLLLQATAILFAVFRYNNHETDALMHNHNSNPONEFYFRYPSFDVHTMTLFGV 74
QY 62 LGFLTSSFRHSHSSVAFNLFMLALGVQMAILLDGLFSLQFPGSKVITLFSIMLATMSAL 121
D 75 FGFLMAFLQRYGSSVGFFLLAFAFALQWSTLVQGFHTFHGGHIGVESMINADFCAG 134
QY 122 SVLISVDVAVLGNVLAQVVMVVLVEVTDLGNLRMTVINSIFNDYHMMNHIVFAAYFGL 161
D 135 AVLISFGAILGKGPADLMLALDEVLFGLINEFVLISLGVKADGSSMTHTFGATFGL 194
QY 182 TVAWCLPKPLPEGTENDQORATIPSLSAMLGAFLMFRPSVNSALLRSPIERKNAVENT 241
D 195 VLSRVLVLPQLSKHRSVYHSDLPFAMIGTLFLMFRPSNSAIPRLDDGQRTALNT 254
QY 242 YAAVAVSVTAISGSSLAHPQGIKSKTYGHSAYLPEGVAVDTSCHLIPSPMLPIVLGLV 301
D 255 YSLTSLTSTFALSALVGRDRLDVHVNQMAALAGVVGTSEMWLTPFGALAAQFLA 314
QY 302 GLISVRGAKY-----LPGCNRLVGTIPHSISIMGNFSLGLLE 339
D 315 GTVSTLGFKEFTPTLSEKFKIQDTCCGVNHLHGPFVGLALLGVVAGLATHDSGEGLES 374
QY 340 EIIVYVLVLDVTGAGNGMIGFOVLSIGELSLAIVALTSGTLTALLNLKIRKAPHEA 399
D 375 -----VPLIAEGGRSSTSQLHQLFGLFTVLIRASVGGIGGLRLPLFDSPPDS 426
QY 400 KYRDDQVFKKP 411
D 427 QCYEDQIYMEVP 438
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RESULT 14

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US-10-369-072-57
; Sequence 57, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alabrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Paturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Raestelli, Luca
; APPLICANT: Grose, William M
; APPLICANT: Szekeres, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shinkets, Richard
; APPLICANT: Padigaru, Muraidhara
; APPLICANT: Paturajan, Meera
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
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/ FILE REFERENCE: 21402-050 CON2
/ CURRENT APPLICATION NUMBER: US/10/369,072
/ PRIOR FILING DATE: 2003-02-18
/ PRIOR APPLICATION NUMBER: 10/174,372
/ PRIOR FILING DATE: 2002-06-17
/ PRIOR APPLICATION NUMBER: 09/898,994
/ PRIOR FILING DATE: 2001-07-03
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/216,585
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ PRIOR FILING DATE: 2000-07-17
/ PRIOR APPLICATION NUMBER: 60/218,992
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 100
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 57
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Sus scrofa
US-10-369-072-57
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Query Match      22.2%; Score 472.5; DB 15; Length 458;
Best Local Similarity 28.9%; Pred. No. 2.5e-35;
Matches 125; Conservative 73; Mismatches 193; Indels 41; Gaps 4;

QY      13 LPLCALTEALAILLFYFTTHY-----DASL-----BDQGVASVYGODLTVMMAIG 61
DB      15 LPLCLFLGATGATVLFVAVRVNHTDAILMHWGNSHPNDEFFFRFSDVHTMTFVG 74
QY      62 LGFTLSFRHSWSVAENLFMLALGVOMAILLDGFLSGFSPGKVITLFSIWLATMSAL 121
DB      75 FEFLLAFQRYGVGSSVGFTEFLAFAFLQWSTLVQGFHLTFPGHGHGVESMINADFCAG 134
QY      122 SVLISVDVAVLGVKNLAQLVWVWLVETDIGNLRVYISNIFPTDYNMMNHITVFAAYFGL 181
DB      135 AVLISFGAILKGTGAQLMLLLEVLVPLGNEFVLISLGVKADAGSMTHTFGAYFGL 194
QY      182 TVAKCLPRLPBGEDNDQATTPSLASMLGALFLMMFRPSVNSALRSPIERKNVAVENT 241
DB      195 VLSRVLYRPLEKSKHRSQSVYHSDLFAMIGTIFLMTFWSPNSAFTPLDQGHRTALNT 254
QY      242 YVAVAVSVVTAISGSSLAHPOGKISKTYGSAVLPBGVAVDTSCHLIPSWLPIVLGLVA 301
DB      255 YSLTASTLSTFLALVGRDGRIDMVVQMAALAGVVVGTSAEMWLTFFGALAAGFLA 314
QY      302 GLISVRGAKY-----LPGCCNRVLGI:PHSSINGVNSLLGLE 339
DB      315 GTVSTLGFKEFTPLIESKFKIOTDTCGVNHLHGWPGVIGALLGVLVAGLATHDSYGEGLS 374
QY      340 EIIYIVLVLDTVANGMIGFOVLISIGELSLAIVIALTSGLLTALLNLKIRKAPHEA 399
DB      375 -----VFFLLAEGRSSSTSQLHQLFVTLIFASVGGIGLLRLRPLDSPPDS 426
QY      400 KYPDQVFWKRP 411
DB      427 QCYEDQIWEVP 438
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RESULT 15
US-10-190-115-55
/ Sequence 55, Application US/10190115
/ Publication No. US20030207394A1
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/ GENERAL INFORMATION:
/ APPLICANT: Alsobrook, John P. II
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Caeman, Stacie J.
/ APPLICANT: Grosse, William M.
/ APPLICANT: Gusev, Vladimir Y.
/ APPLICANT: Ji, Weizhen
/ APPLICANT: Lepley, Denise M.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Merick, Amanda J.
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Racturajan, Meera
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Shen, Lei
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Spaderna, Steven K.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Szekeres, Edward S. Jr.
/ APPLICANT: Taupier, Raymond J. Jr.
/ APPLICANT: Tchernev, Velizar T.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Voss, Edward Z.
/ TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
/ FILE REFERENCE: 21402-050 CIP
/ CURRENT APPLICATION NUMBER: US/10/190,115
/ PRIOR FILING DATE: 2003-02-10
/ PRIOR APPLICATION NUMBER: 60/303,168
/ PRIOR FILING DATE: 2001-07-05
/ PRIOR APPLICATION NUMBER: 60/368,996
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: 60/386,816
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: 60/215,854
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,856
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/215,902
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 60/216,585
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/216,586
/ PRIOR FILING DATE: 2001-07-07
/ PRIOR APPLICATION NUMBER: 60/216,722
/ PRIOR FILING DATE: 2000-07-07
/ PRIOR APPLICATION NUMBER: 60/218,622
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 136
/ SOFTWARE: Curaseq1st version 0.1
/ SEQ ID NO 55
/ LENGTH: 458
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-190-115-55

Query Match      22.0%; Score 466.5; DB 15; Length 458;
Best Local Similarity 29.5%; Pred. No. 9e-35;
Matches 125; Conservative 78; Mismatches 196; Indels 25; Gaps 4;

QY      13 LPLCALTEALAILLFYFTTHY-----DASLDDKG-----LVASVYGODLTVMMAIG 61
DB      15 LPLCLFLGATGATVLFVAVRVNHTDAILMHWGNSHPNDEFFFRFSDVHTMTFVG 74
QY      62 LGFTLSFRHSWSVAENLFMLALGVOMAILLDGFLSGFSPGKVITLFSIWLATMSAL 121
DB      75 FEFLLAFQRYGVGSSVGFTEFLAFAFLQWSTLVQGFHLTFPGHGHGVESMINADFCAG 134
QY      122 SVLISVDVAVLGVKNLAQLVWVWLVETDIGNLRVYISNIFPTDYNMMNHITVFAAYFGL 181
DB      135 AVLISFGAVLKGTPQQLMLLLEVLVPLGNEFVLISLGVKADAGSMTHTFGAYFGL 194
```

QY 182 TVAWCLPKPLPEGTEDNDORATIPSLSAMLGALFLMMFRPSVNSGALLRSPIERKNAVNT 241
Db 195 VLSRVLYRPOLEKSKHROGSVYHSDLPAMIGTIFLWIFWPSFNALATALGAGCHRTALNT 254
QY 242 YYAVAVSVTAISGSLAHPOGKISKTYGHSAYLPEGVAVDTSCHLIPSPWLPYVGLVA 301
Db 255 YYSIAASTLGTFAISALVGEDGRUDMVHIQVPAALAGVVVQTSSEMMILTFPGALAAAGFLA 314
QY 302 GLISVRGAKYLPGCCNRVLGIPIHSSIMGYNFSLLGLEIYYIVLVLDTVGA-GNGMIG 360
Db 315 GTVSTLGYKFFTPILSKFKVQDTGCVHNLHGMPGVLGALLGVLVAGLATHEAYGDLES 374
QY 361 FOYLLSIGE-----LSIAIVIALTSGLTALLNLKIRKAPHAKYFDDQVF 407
Db 375 VFPLIAEGQRSATSQAMHQLFGLFVTLMFASVGGGLGILLKLPFLDSPDSCHYEDQVH 434
QY 408 WKFP 411
Db 435 WQVP 438

Search completed: March 24, 2005, 13:30:00
Job time : 144 secs

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